

65		70		75		80
Ala Tyr Lys Ala	Gly Arg Ala Pro Thr	Pro Glu Asp Phe Pro	Arg Gln			
	85	90	95			
Leu Ala Leu Val	Lys Arg Leu Val	Asp Leu Leu Gly Leu	Val Arg Leu			
	100	105	110			
Glu Ala Pro Gly Tyr	Glu Ala Asp Asp Val	Leu Gly Thr Leu	Ala Lys			
	115	120	125			
Lys Ala Glu Arg Glu Gly	Met Glu Val Arg Ile	Leu Thr Gly Asp Arg				
	130	135	140			
Asp Phe Phe Gln Leu Leu	Ser Glu Lys Val Ser	Val Leu Leu Pro Asp				
	145	150	155			160
Gly Thr Leu Val Thr	Pro Lys Asp Val Gln	Glu Lys Tyr Gly Val	Pro			
	165	170	175			
Pro Glu Arg Trp Val Asp	Phe Arg Ala Leu Thr	Gly Asp Arg Ser Asp				
	180	185	190			
Asn Ile Pro Gly Val Ala Gly	Ile Gly Glu Lys Thr	Ala Leu Arg Leu				
	195	200	205			
Leu Ala Glu Trp Gly Ser	Val Glu Asn Leu Leu	Lys Asn Leu Asp Arg				
	210	215	220			
Val Lys Pro Asp Ser Leu	Arg Arg Lys Ile Glu	Ala His Leu Glu Asp				
	225	230	235			240
Leu His Leu Ser Leu Asp	Leu Ala Arg Ile Arg	Thr Asp Leu Pro Leu				
	245	250	255			
Glu Val Asp Phe Lys Ala	Leu Arg Arg Arg Thr	Pro Asp Leu Glu Gly				
	260	265	270			
Leu Arg Ala Phe Leu Glu	Glu Leu Glu Phe Gly	Ser Leu Leu His Glu				
	275	280	285			
Phe Gly Leu Leu Gly Gly	Glu Lys Pro Arg Glu	Glu Ala Pro Trp Pro				
	290	295	300			
Pro Pro Glu Gly Ala Phe	Val Gly Phe Leu Leu	Ser Arg Lys Glu Pro				
	305	310	315			320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Glu Gly Arg Val
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460

Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525

Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
 770 775 780

Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu
 785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala

820

825

830

Lys Gln Asp
835

<210> 342

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 342

tggcggcggc ctcgggcggc cgcgtccacc gggcaaca

38

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 343

cttctctcat ccgccaaaac agcc

24

<210> 344

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 344

tggccgcccgc ctggggcggc cgcgtttacc gggcggag

38

<210> 345

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 345

```
atgaattcca ccccactttt tgacctggag gaacccccca agcgggtgct tctggtggac      60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag      120
ccggtgcaga tggctctacg cttcgccccg agcctcctca aggccttgaa ggaggacgga      180
caggcggtgg tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggacctacgag      240
gcctacaagg cgggcccgggc cccacccccg gaggacttcc ccgcccagct cgccttggtc      300
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac      360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcatactc      420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac      480
gggaccttg tcccccaaa ggacgtccag gagaagtacg gggtgcccc ggagcgctgg      540
gtggacttcc gcgccctcac ggggggaccgc tcggacaaca tccccggggg ggccggggata      600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag      660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac      720
ctccacctct ccttagacct ggcccgcac cgcaccgacc tccccctgga ggtggacttt      780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg      840
gagttcggaa gcctcctcca cgagttcggc ctcttgggag gggagaagcc ccgggaggag      900
gccccctggc ccccgcccga aggggccttc gtgggcttcc tcctttcccg caaggagccc      960
atgtgggcgg agcttctggc cctggcgggc gcctcggggc gccgcgtcca ccgggcaaca     1020
agcccggttg aggccttggc cgacctcaag gaggcccggg ggttcctggc caaggacctg     1080
gccgttttgg ccctgcggga ggggggtggcc ctggacccca cggacgaccc cctcctggtg     1140
gcctacctcc tggacctggc caacacccac cccgaggggg tggcccggcg ctacggggggc     1200
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggtctt ccagaacctc     1260
tttaaacggc tttccgagaa gctcctctgg ctctaccagg aggtggagcg gccccctctcc     1320
cgggtcttgg ccacatgga gggccggggg gtgaggctgg acgtccccct tctggaggcc     1380
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc     1440
ggccaccctc tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg     1500
```

ggccacccc cgggtgggccc gacgcagaag acgggcaagc gctccaccgc ccagggggccc 1560
 ctggaggccc tccggggggc ccaccccatc gtggagctca tcctccagta ccgggagctt 1620
 tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccaccg gcggacgggc 1680
 cggtccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac 1740
 cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcatccg caaggccttc 1800
 gtggccgagg aggggtggct ccttttggcg gcggactact cccagattga gctccgggtc 1860
 ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc 1920
 cataccgaga ccgcgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg 1980
 cgccggggcg ccaagacggc caacttcggc gtccctctacg ggatgtccgc ccacaggctc 2040
 tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag 2100
 agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc 2160
 tacgtggaga ccctgttcgg caggaggcgc tatgtgcccc acctggcctc ccgggtccgc 2220
 tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggccac 2340
 ctctcctcc aagtgcacaa cgagctggtc ctggaggtgc ccgaggaccg ggccgaggag 2400
 gccaaggccc tggtaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag 2460
 gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggat 2505

<210> 346

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 346

Met	Asn	Ser	Thr	Pro	Leu	Phe	Asp	Leu	Glu	Glu	Pro	Pro	Lys	Arg	Val
1				5					10					15	

Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		

Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe
		35					40					45			

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460

Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525

Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly

545					550						555				560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
				565					570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Lys	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Leu	Leu
		595					600					605			
Leu	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Lys	Arg	Val	Phe	Arg	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Glu	Thr	Ala	Ala	Trp	Met	Phe	Gly	Leu	Asp	Pro	Ala	Leu	Val
				645					650					655	
Asp	Pro	Lys	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Gly	Ile	Asp	Tyr
		675					680					685			
Lys	Glu	Ala	Glu	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Arg	Thr	Leu	Glu	Glu	Gly	Arg	Thr	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala
				725					730					735	
Ser	Arg	Val	Arg	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Ile	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Lys	Pro	Leu	Gly	Ala	His	Leu	Leu	Leu	Gln
	770					775					780				
Val	His	Asn	Glu	Leu	Val	Leu	Glu	Val	Pro	Glu	Asp	Arg	Ala	Glu	Glu
785					790					795					800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala
820 825 830

Lys Gln Asp
835

<210> 347

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 347

atgaattccc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggcccc tccttccgcc accagacctt cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaagaa gaaggctacg aagtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcaccc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac	540
taccgggcct tggccgggga cccttcgcac aacatccccg gcgtgaaggg catcggggag	600
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg	660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720
ctatccctgg agctatcccc ggtgcacacg gacttgctcc ttcaggtgga cttcgccccg	780
cgccggggagc cggaccggga ggggcttaag gccttttttg agaggctgga gttcggaagc	840
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg	900
ccccccgagg gagccttcgt ggggtacgtt ctttccccgc ccgagcccat gtgggcggag	960
cttaacgcct tggccgccgc ctggggcggc cgcgtttacc gggcggagga tcccttgag	1020
gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc	1080

ctgaggggaag ggattgccct ggcaccgggc gacgacccca tgctcctcgc ctacctcctg	1140
gataccttcca acaccgcccc cgaaggggta gcccggcgct acgggggggga gtggaccgag	1200
gaggcggggg aaagggcgct gctttccgaa aggcctttacg ccgccctcct gaagcggtt	1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc	1320
ctggcccaca tggaggccac ggggggtacgg ttggatgtgg cctacttaaa ggccctttcc	1380
ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat	1440
cctttcaacc tgaactcccg ggaccagctg gaaaggggtca tctttgacga gcttgggctt	1500
cccgccatcg gcaagacgca gaagacgggc aagcgctcca ccagcgccgc cgttttggag	1560
gccttgcggg aggtcatcc catcgtggac cgcataccttc agtaccggga gctttccaag	1620
ctcaagggaa cctacatcga tcccttgccct gccctgggtcc accccaagac gaaccgcctc	1680
cacaccggtt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatccta	1740
ctgcaaaata tccccgtgcg caccctttg ggccagcgga tccgcccggc cttcgtggcc	1800
gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg	1860
cacctttccg gggacgagaa cctaataccg gtcttccagg agggccagga catccacacc	1920
cagacggcca gctggatgtt cggcgtgccc ccagaggccg tggattccct gatgcgccg	1980
gcggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcggga	2040
gagctggcca tccccctacga ggaggcggtg gccttcatcg agcgggtattt ccagagctac	2100
cccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg	2160
gaaaccctct ttggccgccg gcgctacgtg ccgacttgg cttcccgggt gaagagcatc	2220
cgggaggcag cggagcgcac ggccttcaac atgccggtcc aggggaccgc cgcggatttg	2280
atgaaactgg ccatggtgaa gctctttccc aggccttcagg agctgggggc caggatgctt	2340
ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc	2400
caggaggcca agcggaccat ggaggaggtg tggccctga aggtgccctt ggaggtggaa	2460
gtgggcatcg gggaggactg gctttccgcc aaggcc	2496

<210> 348

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 348

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys
	210					215					220				
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys
225					230					235					240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu
 325 330 335
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu
 405 410 415
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu
 450 455 460
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp
 485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr
 530 535 540

Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr
 625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670

Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg
 690 695 700

Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val
 705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg
 725 730 735

Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro

740		745		750											
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
	755						760					765			
Phe	Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
	770					775					780				
Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val	Ala
785					790					795					800
Gln	Glu	Ala	Lys	Arg	Thr	Met	Glu	Glu	Val	Trp	Pro	Leu	Lys	Val	Pro
			805						810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Ala
		820						825					830		

<210> 349

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 349

atgaattcca	ccccactttt	tgacctggag	gaacccccca	agcgggtgct	tctggtggac	60
ggccaccacc	tggcctaccg	caccttctat	gccctgagcc	tcaccacctc	ccgggggggag	120
ccggtgcaga	tgggtctacg	cttcgcccgg	agcctcctca	aggccttgaa	ggaggacgga	180
caggcggtgg	tcgtggtctt	tgacgccaag	gccccctcct	tccgccacga	ggcctacgag	240
gcctacaagg	cgggcccggg	ccccaccccg	gaggacttcc	cccgccagct	cgccttggtc	300
aagcggctgg	tggaccttct	gggctttacc	cgcctcgagg	ccccggggta	cgaggcggac	360
gacgtcctgg	gcaccctggc	caagaaggcc	gaaagggagg	ggatggaggt	gcgcatacct	420
acgggagacc	gggacttctt	ccagctcctc	tccgagaagg	tctcggtcct	cctgccggac	480
gggaccctgg	tcacccccaa	ggacgtccag	gagaagtacg	gggtgcccc	ggagcgctgg	540
gtggacttcc	gcgccctcac	gggggaccgc	tccgacaaca	tccccgggg	ggcggggata	600
ggggagaaga	ccgcccttcg	actcctcgca	gagtggggga	gcgtggaaaa	cctcctgaag	660
aacctggacc	gggtaaagcc	ggactcgctc	cggcgcaaga	tagaggcgca	cctcgaggac	720

ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt	780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg	840
gagttcggaa gcctcctcca cgagttcggc ctcttgggag gggagaagcc ccgggaggag	900
gccccctggc ccccgcccgga aggggccttc gtgggcttcc tcctttcccg caaggagccc	960
atgtgggcgg agcttctggc cctggcgggc gcctcggggc gccgcgtcca ccgggcaaca	1020
agcccggttg aggccttggc ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccg gggacgaccc catgctcctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccttacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg	1680
acgggcgcgc tcacaccccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg ccacctctc cggggacgaa aacctgatca gggctctcca ggaggggag	1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctc tctacggcat gtcgcgccat	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccaaagt gcgggccttg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacct caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcggggc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 350

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 350

```
atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac      60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccggggggag      120
ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180
caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag      240
gcctacaagg cgggccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc      300
aagcggtctg tggaccttct gggctttacc cgcctcgagg ccccggggta cgaggcggac      360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcatactc      420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac      480
gggaccctgg tcacccccaa ggacgtccag gagaagtacg gggtgccccg ggagcgctgg      540
gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccggggg ggcggggata      600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag      660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac      720
ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt      780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg      840
gagttcggaa gcctcctcca cgagttcggc ctcttgaggag gggagaagcc ccgggaggag      900
gccccctggc ccccgccga aggggccttc gtgggcttcc tcctttcccg caaggagccc      960
atgtgggcgg agcttctggc cctggcgggc gcctcgggcg gccgcgtcca ccgggcaaca     1020
agcccgggtg aggccttggc cgacctcaag gagggccggg ggttcctggc caaggacctg     1080
gccgttttgg cctgcggga gggggtggcc ctggacccca cggacgaccc cctcctggtg     1140
gcctacctcc tggaccggc caacaccac cccgaggggg tggcccggcg ctacgggggc     1200
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc     1260
tttaaacggc tttccgagaa gctcctctgg ctctaccagg aggtggagcg gccctctcc     1320
cgggtcttgg ccacatgga ggccccgggg gtgaggctgg acgtccccct tctggaggcc     1380
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc     1440
```

ggccacccct tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg 1500
 ggcctcaccc cggtggggccg gacgcagaag acgggcaagc gctccaccgc ccagggggcc 1560
 ctggaggccc tccggggggc ccaccccatc gtggagctca tctccagta ccgggagctt 1620
 tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccaccc gcggacgggc 1680
 cggtccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac 1740
 cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc 1800
 gtggccgagg aggggtggct ccttttggcg gcggactact ccagattga gctccgggtc 1860
 ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc 1920
 cataccgaga ccgccgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg 1980
 cgccggggcg ccaagacggt caacttcggc gtctctacg ggatgtccgc ccacaggctc 2040
 tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag 2100
 agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc 2160
 tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc ccgggtccgc 2220
 tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac 2340
 ctctcctcc aagtgcacaa cgagctggtc ctggaggtgc ccgaggaccg ggccgaggag 2400
 gccaaagccc tggtaagga ggtcatggag aacgcctacc ccctggacgt gccctcgag 2460
 gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggat 2505

<210> 351

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 351

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
 20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe

35	40	45																	
Ala	Arg	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Gln	Ala	Val	Val				
50						55					60								
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu				
65					70					75					80				
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln				
				85					90					95					
Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu				
			100					105					110						
Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	Lys				
		115					120					125							
Lys	Ala	Glu	Arg	Glu	Gly	Met	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg				
130						135					140								
Asp	Phe	Phe	Gln	Leu	Leu	Ser	Glu	Lys	Val	Ser	Val	Leu	Leu	Pro	Asp				
145					150					155					160				
Gly	Thr	Leu	Val	Thr	Pro	Lys	Asp	Val	Gln	Glu	Lys	Tyr	Gly	Val	Pro				
				165					170					175					
Pro	Glu	Arg	Trp	Val	Asp	Phe	Arg	Ala	Leu	Thr	Gly	Asp	Arg	Ser	Asp				
			180					185					190						
Asn	Ile	Pro	Gly	Val	Ala	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Arg	Leu				
		195					200					205							
Leu	Ala	Glu	Trp	Gly	Ser	Val	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg				
	210					215					220								
Val	Lys	Pro	Asp	Ser	Leu	Arg	Arg	Lys	Ile	Glu	Ala	His	Leu	Glu	Asp				
225					230					235					240				
Leu	His	Leu	Ser	Leu	Asp	Leu	Ala	Arg	Ile	Arg	Thr	Asp	Leu	Pro	Leu				
				245					250					255					
Glu	Val	Asp	Phe	Lys	Ala	Leu	Arg	Arg	Arg	Thr	Pro	Asp	Leu	Glu	Gly				
			260					265						270					
Leu	Arg	Ala	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu				
		275					280					285							

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
325 330 335
His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
340 345 350
Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
355 360 365
Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
370 375 380
Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
420 425 430
Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
435 440 445
Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
450 455 460
Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
465 470 475 480
Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
485 490 495
Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly
500 505 510
Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
515 520 525
Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655
 Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
 770 775 780
 Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu

785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala
820 825 830

Lys Gln Asp
835

<210> 352

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 352

atgaattccc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acggggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagacctt cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttcccgcgc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt taccgcctc gaggtgcgcg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcaccc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac	540
taccgggcct tggccgggga cccttcgcgc aacatccccg gcgtgaaggc catcggggag	600
aagacggcgc ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg	660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720
ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg	780
cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcgggaagc	840
ctcctccacg agttcggcct gttggaaaag ccggtggcgc cggaggaagc tccctggccg	900
ccccccgagg gagccttcgt ggggtacgtt ctttcccgc cggagcccat gtgggcggag	960

cttaacgcct tggccgccgc ctggggcggc cgcgtttacc gggcggagga tcccttggag	1020
gccttgcggg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc	1080
ctgaggggaag ggattgccct ggcaccgggc gacgacccca tgctcctcgc ctacctcctg	1140
gataccttcca acaccgcccc cgaaggggta gcccggcgct acggggggga gtggaccgag	1200
gaggcggggg aaagggcgct gctttccgaa aggcctttacg ccgccctcct gaagcggcctt	1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc	1320
ctggcccaca tggaggccac ggggggtacgg ttggatgtgg cctacttaaa ggccctttcc	1380
ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat	1440
cctttcaacc tgaactcccg ggaccagctg gaaaggggtca tctttgacga gcttgggctt	1500
cccgccatcg gcaagacgca gaagacgggc aagcgctcca ccagcgccgc cgttttggag	1560
gccttgcggg aggcctcatcc catcgtggac cgcaccttc agtaccggga gctttccaag	1620
ctcaagggaa cctacatcga tcccttgctt gccctgggtcc accccaagac gaaccgcctc	1680
cacaccggtt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatcctaata	1740
ctgcaaaaata tccccgtgcg cacccttttg ggccagcgga tccgccgggc ctctgtggcc	1800
gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg	1860
cacctttccg gggacgagaa cctaataccg gtcttccagg agggccagga catccacacc	1920
cagacggcca gctggatggt cggcgtgccc ccagaggccg tggattccct gatgcgccgg	1980
gcggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcgga	2040
gagctggcca tccccctacga ggaggcgggt gccttcatcg agcgggtattt ccagagctac	2100
cccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg	2160
gaaaccctct ttggccgccc gcgctacgtg cccgacttgg cttcccgggt gaagagcatc	2220
cgggaggcag cggagcgcct ggccttcaac atgccggtcc aggggaccgc cgcggatttg	2280
atgaaactgg ccatggtgaa gctctttccc aggccttcagg agctgggggc caggatgctt	2340
ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtgcgc	2400
caggaggcca agcggaccat ggaggaggtg tggccccctga aggtgccctt ggaggtggaa	2460
gtgggcatcg gggaggactg gctttccgcc aaggcc	2496

<210> 353

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 353

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240
 Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu
 325 330 335
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu
 405 410 415
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu
 450 455 460
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg

	725		730		735
Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro					
	740		745		750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu					
	755		760		765
Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His					
	770		775		780
Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala					
	785		790		800
Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro					
	805		810		815
Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala					
	820		825		830

<210> 354
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 354
 ggccctcacc cgggtgaagcg gacgaagaag acgggcaagc gc

42

<210> 355
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 355
 gcgccttgcgc gtctttcttcg tccgcttcac cgggggtgagg cc

42

<210> 356
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 356
 ctctctctcc aagtggccaa cgagctgggc ctg 33

<210> 357
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 357
 caggaccagc tcgttggcca cttggaggag gag 33

<210> 358
 <211> 2505
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 358
 atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60
 ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120
 ccggtgcaga tggctctacgg cttcgcccg agcctcctca aggccttgaa ggaggacgga 180
 caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240
 gcctacaagg cgggcccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300
 aagcggctgg tggaccttct gggcctgggc cgcctcgagg ccccggggta cgaggcggac 360

gacgtcctgg gcaccctggc caagaaggcc gaaagggagg ggatggaggt gcgcatactc	420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac	480
gggaccctgg tcaccccaaa ggacgtccag gagaagtacg gggtgccccc ggagcgctgg	540
gtggacttcc gcgcctcac gggggaccgc tcggacaaca tccccggggt ggcggggata	600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag	660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac	720
ctccacctct ccttagacct ggcccgcata cgcaccgacc tccccctgga ggtggacttt	780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg	840
gagttcggaa gcctcctcca cgagttcggc ctcttgggag gggagaagcc ccgggaggag	900
gccccctggc ccccgcccgga aggggccttc gtgggcttcc tcctttcccg caaggagccc	960
atgtggggcg agcttctggc cctggcgggc gcctcggggc gccgcgtcca ccgggcaaca	1020
agcccggttg aggccctggc cgacctcaag gagggccggg ggttctctggc caaggacctg	1080
gccgttttgg cctgcggga ggggggtggc ctggaccca cggacgaccc cctcctggtg	1140
gcctacctcc tggacccggc caacacccac cccgaggggg tggcccgggc ctacgggggc	1200
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc	1260
tttaaacggc tttccgagaa gctcctctgg ctctaccagg aggtggagcg gcccctctcc	1320
cgggtcttgg ccacatgga ggcccgggg gtgaggctgg acgtccccct tctggaggcc	1380
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc	1440
ggccacccct tcaacctcaa ctcccgcgac cagctggaaa gggctcctct tgacgagctg	1500
ggcctcacc cgggtgaagcg gacgaagaag acgggcaagc gctccaccgc ccagggggcc	1560
ctggaggccc tccggggggc ccaccccatc gtggagctca tcctccagta ccgggagctt	1620
tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccacc gcggacgggc	1680
cggctccaca ccgcttcaa ccagacggc acggccacgg gaaggctttc cagctccgac	1740
cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc	1800
gtggccgagg aggggtggct ccttttggcg gcggactact ccagattga gctccgggtc	1860
ctggccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc	1920
cataccgaga ccgccgcctg gatgttcggc ttagaccccc ctctggtgga tccaaagatg	1980
cgcggggcgg ccaagacggc caacttcggc gtcctctacg ggatgtccgc ccacaggctc	2040
tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag	2100
agcttcccca aggtgcgggc ctggatagaa aggacctgg aggagggccg gacgcggggc	2160
tacgtggaga ccctgttcgg caggaggcgc tatgtgccc acctggcctc ccgggtccgc	2220

tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggccac 2340
ctcctectcc aagtggccaa cgagctggtc ctggaggtgc ccgaggaccg ggccgaggag 2400
gccaaggccc tggtaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag 2460
gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggat 2505

<210> 359

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 359

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160

Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175

Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190

Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205

Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255

Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val

<223> Synthetic

<400> 360

gggcttcccg ccatcaagaa gacgaagaag acgggcaagc gc

42

<210> 361

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 361

gcgcttgccc gtcttcttcg tcttcttgat ggcgggaagc cc

42

<210> 362

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 362

atgcttttgc aggtggccaa cgaactggtc ctc

33

<210> 363

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 363

gaggaccagt tcgttgcca cctgcaaaag cat

33

<210> 364

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 364

```
atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac      60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc      120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagacctt cgaggcctac      240
aaggcggggc gggctccac ccccgaggac tttcccgcgc agcttgccct tatcaaggag      300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg      420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac      480
ctgatcaccc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac      540
taccgggcct tggccgggga cccttcgcgc aacatccccg gcgtgaaggc catcggggag      600
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg      660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag      720
ctatccctgg agctatcccc ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg      780
cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcggaagc      840
ctcctccacg agttcggcct gttggaaaag ccggtggcgg cggaggaagc tccctggccg      900
cccccgagg gagccttcgt ggggtacgtt ctttccgcgc ccgagcccat gtgggcggag      960
cttaacgcct tggccgccgc ctggggcggc gcgctttacc gggcggagga tcccttgagag      1020
gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc      1080
ctgagggaag ggattgccct ggcaccgggc gacgaccca tgctcctcgc ctacctcctg      1140
gatccttcca acaccgcccc cgaaggggta gcccgcgct acggggggga gtggaccgag      1200
gaggcggggg aaaggcgct gctttccgaa aggctttacg ccgccctcct gaagcggcct      1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc      1320
ctggcccaca tggaggccac gggggctacg ttggatgtgg cctacttaaa ggccctttcc      1380
ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat      1440
cctttcaacc tgaactcccc ggaccagctg gaaagggtca tctttgacga gcttgggctt      1500
```

cccgccatca agaagacgag gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560
 gccttgcggg aggtcatcc catcgtggac cgcaccttc agtaccggga gctttccaag 1620
 ctcaagggaa cctacatcga tcccttgctt gccctggtcc accccaagac gaaccgcctc 1680
 cacacccgtt tcaaccagac ggccaccgcc acggggagggc ttagcagctc ggatcctaata 1740
 ctgcaaaata tccccgtgcg cacccttttg ggccagcgga tccgcggggc cttcgtggcc 1800
 gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg 1860
 cacctttccg gggacgagaa cctaatacgg gtcttcagg agggccagga catccacacc 1920
 cagacggcca gctggatgtt cggcgtgccc ccagaggccg tggattccct gatgcgccgg 1980
 ggggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcggga 2040
 gagctggcca tccccctacga ggaggcggtg gccttcatcg agcggtatatt ccagagctac 2100
 cccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg 2160
 gaaaccctct ttggccgccc gcgctacgtg cccgacttgg cttcccgggt gaagagcatc 2220
 cgggaggcag cggagcgcat ggccctcaac atgccggtcc aggggaccgc cgcggatttg 2280
 atgaaactgg ccatggtgaa gctctttccc aggccttcagg agctgggggc caggatgctt 2340
 ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400
 caggaggcca agcggaccat ggaggaggtg tggcccctga aggtgccctt ggaggtggaa 2460
 gtgggcatcg gggaggactg gctttccgcc aaggcc 2496

<210> 365

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 365

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10				15		

Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
 130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
 145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu
 325 330 335
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu
 405 410 415
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu
 450 455 460
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu

545					550										555				560
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser				
				565					570					575					
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln				
			580					585					590						
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	Val				
	595						600					605							
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly				
	610					615					620								
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	Thr				
625					630					635					640				
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Ser				
				645					650						655				
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly				
			660					665					670						
Met	Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu				
		675					680					685							
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg				
	690					695					700								
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Ala	Glu	Gly	Arg	Glu	Arg	Gly	Tyr	Val				
705					710					715					720				
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala	Ser	Arg				
				725					730					735					
Val	Lys	Ser	Ile	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro				
			740					745					750						
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu				
		755					760					765							
Phe	Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His				
	770					775					780								
Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val	Ala				
785					790					795					800				

Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala
820 825 830

<210> 366

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 366

atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac	60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag	120
ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga	180
caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag	240
gcctacaagg cgggcccgggc ccccaacccg gaggacttcc cccgccagct cgccttggtc	300
aagcggctgg tggaccttct gggctttacc cgcctcgagg ccccggggta cgaggcggac	360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcctcctc	420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac	480
gggaccctgg tcacccccaa ggacgtccag gagaagtacg ggggtgcccc ggagcgctgg	540
gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccggggt ggcggggata	600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag	660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac	720
ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt	780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg	840
gagttcggaa gcctcctcca cgagttcggc ctctctggag gggagaagcc ccgggaggag	900
gccccctggc ccccgcccgga aggggccttc gtgggcttcc tcctttcccg caaggagccc	960
atgtgggcgg agcttctggc cctggcggcg gcctcgggag gccgcgtcca ccgggcaaca	1020
agcccggttg aggccttggc cgacctcaag gagggccggg ggttcctggc caaggacctg	1080
gccgttttgg ccctgcggga gggggtggcc ctggacccca cggacgacct cctcctggtg	1140
gcctacctcc tggaccggc caacaccac cccgaggggg tggcccgcg ctacgggggg	1200

gagttcacgg	aggacgcagc	ggagagggcc	ctcctctccg	agaggctctt	ccagaacctc	1260
tttaaacggc	tttccgagaa	gctcctctgg	ctctaccagg	aggtggagcg	gcccctctcc	1320
cgggtcttgg	cccacatgga	ggcccggggg	gtgaggttgg	acgtccccct	tctggaggcc	1380
ctctcctttg	agctggagaa	ggagatggag	cgcctggagg	gggaggtctt	ccgtttggcc	1440
ggccaccctt	tcaacctcaa	ctcccgcgac	cagctggaaa	gggtcctctt	tgacgagctg	1500
ggcctcacc	cggatgaagc	gacgaagaag	acgggcaagc	gctccaccgc	ccagggggcc	1560
ctggaggccc	tccggggggc	ccaccccatc	gtggagctca	tcctccagta	ccgggagctt	1620
tccaagctca	aaagcaccta	cctggacccc	ctgccccggc	tcgtccacc	gcggacgggc	1680
cggctccaca	cccgttcaa	ccagacggcc	acggccacgg	gaaggctttc	cagctccgac	1740
cccaacctgc	agaacatccc	cgtgcgcacc	cccttggggc	agcgcacccg	caaggccttc	1800
gtggccgagg	aggggtggct	ccttttggcg	gcggactact	cccagattga	gctccgggtc	1860
ctggcccacc	tctcggggga	cgagaacctg	aagcgggtct	tccgggaggg	gaaggacatc	1920
cataccgaga	ccgccgcctg	gatgttcggc	ttagaccccg	ctctggtgga	tccaaagatg	1980
cgccgggagg	ccaagacggt	caacttcggc	gtcctctacg	ggatgtccgc	ccacaggctc	2040
tcccaggagc	tcggcataga	ctacaaggag	gcggaggcct	ttattgagcg	ctacttccag	2100
agcttcccca	aggtgcgggc	ctggatagaa	aggaccctgg	aggagggccg	gacgcggggc	2160
tacgtggaga	ccctgttcgg	caggaggcgc	tatgtgcccg	acctggcctc	ccgggtccgc	2220
tcggtgcggg	aggcggcgga	gcggatggcc	ttcaacatgc	ccgtgcaggg	caccgccgcc	2280
gacctgatga	agatcgccat	ggtcaagctc	ttccccaggc	taaagcccct	ggggggccac	2340
ctcctcctcc	aagtggccaa	cgagctggtc	ctggaggtgc	ccgaggaccg	ggccgaggag	2400
gccaaggccc	tggtcaagga	ggtcatggag	aacgcctacc	ccctggacgt	gcccctcgag	2460
gtggaggtgg	gcgtgggtcg	ggactggctg	gaggcgaagc	aggat		2505

<210> 367

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 367

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val

1		5						10						15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		
Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Arg	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Gln	Ala	Val	Val
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65					70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	
Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Arg	Glu	Gly	Met	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg
	130					135					140				
Asp	Phe	Phe	Gln	Leu	Leu	Ser	Glu	Lys	Val	Ser	Val	Leu	Leu	Pro	Asp
145					150					155					160
Gly	Thr	Leu	Val	Thr	Pro	Lys	Asp	Val	Gln	Glu	Lys	Tyr	Gly	Val	Pro
				165					170					175	
Pro	Glu	Arg	Trp	Val	Asp	Phe	Arg	Ala	Leu	Thr	Gly	Asp	Arg	Ser	Asp
			180					185					190		
Asn	Ile	Pro	Gly	Val	Ala	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Arg	Leu
		195					200					205			
Leu	Ala	Glu	Trp	Gly	Ser	Val	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Asp	Ser	Leu	Arg	Arg	Lys	Ile	Glu	Ala	His	Leu	Glu	Asp
225					230					235					240
Leu	His	Leu	Ser	Leu	Asp	Leu	Ala	Arg	Ile	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	

Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460

Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525

Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val

755		760		765											
Lys	Leu	Phe	Pro	Arg	Leu	Lys	Pro	Leu	Gly	Ala	His	Leu	Leu	Leu	Gln
770						775					780				
Val	Ala	Asn	Glu	Leu	Val	Leu	Glu	Val	Pro	Glu	Asp	Arg	Ala	Glu	Glu
785					790					795					800
Ala	Lys	Ala	Leu	Val	Lys	Glu	Val	Met	Glu	Asn	Ala	Tyr	Pro	Leu	Asp
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Val	Gly	Arg	Asp	Trp	Leu	Glu	Ala
			820					825					830		
Lys	Gln	Asp													
		835													

<210> 368

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 368	
atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcg ggagccggtc	120
caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggcccc tccttcgcgc accagaccta cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac	540
taccgggcct tggccgggga cccttcgcac aacatccccg gcgtgaaggg catcggggag	600
aagacggcgg ccaagctgat ccgggagtg ggaagcctgg aaaaccttct taagcacctg	660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720

ctatccctgg agctatcccc ggtgcacacg gacttgtctc ttcaggtgga cttcgcccgg	780
cgccgggagc cggaccggga ggggcttaag gccttttttg agaggctgga gttcggaagc	840
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg	900
ccccccgagg gagccttcgt ggggtacgtt ctttcccgc cagagcccat gtgggcggag	960
cttaacgcct tggccgccgc ctggggcggc cgcgtttacc gggcggagga tcccttgag	1020
gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc	1080
ctgaggggaag ggattgccct ggcaccgggc gacgacccca tgctcctcgc ctacctcctg	1140
gacctttcca acaccgcccc cgaaggggta gcccggcgt acggggggga gtggaccgag	1200
gaggcggggg aaagggcgct gctttccgaa aggctttacg ccgccctcct gaagcggcct	1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc	1320
ctggcccaca tggaggccac ggggggtacg ttggatgtgg cctacttaaa ggccctttcc	1380
ctggaggtgg aggcgagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat	1440
cctttcaacc tgaactcccg ggaccagctg gaaagggta tctttgacga gcttgggctt	1500
cccgccatca agaagacgag gaagacgggc aagcgtcca ccagcgccgc cgttttgag	1560
gccttgccgg aggctcatcc catcgtggac cgcctccttc agtaccggga gctttccaag	1620
ctcaaggga cctacatcga tcccttgctt gccctggtcc accccaagac gaaccgcctc	1680
cacaccgctt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatccta	1740
ctgcaaaata tccccgtgcg caccctttg ggccagcgga tccgcccggc cttcgtggcc	1800
gaggaggggt ggaggctggt ggttttgac tacagccaga ttgagctcag ggtcctggcg	1860
cacctttccg gggacgagaa cctaaccgg gtcttccagg agggccagga catccacacc	1920
cagacggcca gctggatgtt cggcgtgccc ccagaggccg tggattccct gatgcgccg	1980
gcgccaaga ccatcaactt cggcgtcctc tacggcatgt ccgccaccg gctttcggga	2040
gagctggcca tcccctacga ggaggcggtg gccttcatcg agcggtatct ccagagctac	2100
cccaagggtg gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg	2160
gaaaccctct ttggccgccg gcgctacgtg cccgacttgg cttcccgggt gaagagcatc	2220
cgggaggcag cggagcgcat ggccttcaac atgccggtcc aggggaccgc cgcggatttg	2280
atgaaactgg ccatggtgaa gctctttccc aggcttcagg agctgggggc caggatgctt	2340
ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc	2400
caggaggcca agcggaccat ggaggaggtg tggccctga aggtgccctt ggaggtggaa	2460
gtgggcatcg gggaggactg gctttccgcc aaggcc	2496

<210> 369

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 369

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu
 325 330 335

Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380

Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400

Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu
 405 410 415

Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu
 450 455 460

Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp
 485 490 495

Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr
 530 535 540

Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr
 625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670

Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg

<220>

<223> Synthetic

<400> 371

ccctccgaca acctcaaggg ggtcaagggc atc

33

<210> 372

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 372

gaggttgtcg gaggggtc

18

<210> 373

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 373

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagg acttccccgc gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcgcg acaacctcgc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660

ctcaagaacc	tggaaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcgggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	ccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtggggcg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gacctccttg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggaaccttc	gaacaccacc	cccagggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcgaggagg	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	acctcttcaa	cctcaactcc	cgggaccagc	tggaaagggg	gctctttgac	1500
gagcttaggc	ttcccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acggggccgcc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tcgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggcccagag	gatccgccgg	1800
gccttcgtgg	cagaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcgggcaa	gacgggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaagg	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatagaagc	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggagggtg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggagggtg	aggtggggat	gggggaggac	tggctttccg	ccaaggggtc	ccaccaccac	2520

caccac

2526

<210> 374

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Ala Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile

675	680	685
Pro Tyr Glu Glu Ala Val	Ala Phe Ile Glu Arg	Tyr Phe Gln Ser Phe
690	695	700
Pro Lys Val Arg Ala Trp	Ile Glu Lys Thr Leu	Glu Glu Gly Arg Lys
705	710	715
Arg Gly Tyr Val Glu Thr	Leu Phe Gly Arg Arg	Arg Tyr Val Pro Asp
725	730	735
Leu Asn Ala Arg Val Lys	Ser Val Arg Glu Ala Ala	Glu Arg Met Ala
740	745	750
Phe Asn Met Pro Val Gln	Gly Thr Ala Ala Asp	Leu Met Lys Leu Ala
755	760	765
Met Val Lys Leu Phe Pro	Arg Leu Arg Glu Met	Gly Ala Arg Met Leu
770	775	780
Leu Gln Val Ala Asn Glu	Leu Leu Leu Glu Ala	Pro Gln Ala Arg Ala
785	790	795
Glu Glu Val Ala Ala Leu	Ala Lys Glu Ala Met	Glu Lys Ala Tyr Pro
805	810	815
Leu Ala Val Pro Leu Glu	Val Glu Val Gly Met	Gly Glu Asp Trp Leu
820	825	830
Ser Ala Lys Gly His His	His His His	
835	840	

<210> 375

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120

gaaccggtgc	aggcggtcta	cggttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaaggccc	cctccttcog	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgaggcccc	cggtacgag	360
gcggaacgac	ttctcgccac	cctggccaag	aaggcggaag	aggaggggta	cgagggtgcg	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgtcctccac	480
cccaggggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttcgcgc	cctcgtgggg	gacccctccg	acaacctcaa	gggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggtgctgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaaccg	gaggggctta	gggccttcc	ggagaggctg	840
gagttcgga	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcggga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagggggg	tggcgcgggc	ctacgggggg	1200
gagtggaagg	aggacgcgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgagggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accgggttac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttcgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	agaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccaccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgaccca	acctgcagaa	catccccgtc	cgcacccctt	tgggcccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980

ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagt gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcact caacgcccgg 2220
 gtgaagagcg tcaggaggcg cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gccgcgatgc tcctccaggt cgccaacgag ctctccttg aggcccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 376

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 376

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr

100	105	110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		
115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		
130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His		
145	150	155
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		
165	170	175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		
180	185	190
Ser Asp Asn Leu Lys Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		
195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		
210	215	220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu		
225	230	235
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu		
245	250	255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly		
260	265	270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu		
275	280	285
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro		
290	295	300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro		
305	310	315
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val		
325	330	335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val		
340	345	350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 377

<211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 377
 gagaggctcc atcggaagaa gcttaagcgc ctcgag 36

 <210> 378
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 378
 ccgatggagc ctctccga 18

 <210> 379
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 379
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420

atcctcaccg	ccgaccgcga	cctctacca	ctcgtctccg	accgcgtcgc	cgctctccac	480
cccaggggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaaccg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcggga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagagggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaagaag	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgccct	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccccc	cccacgtggg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctccc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccc	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgccccat	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaagg	gcgggcctgg	atagaaaaga	ccctggagga	ggggagggaag	2160
cggggctacg	tggaaacctc	cttcggaaga	aggcgctacg	tgcccgacct	caacgccccg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280

gcccgcgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcgatgc tcctccaggt cgccaacgag ctctctctgg aggcccccca agcgcggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 380

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 380

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Lys Lys Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu

<223> Synthetic

<400> 381

gtgcgacacg acctcctcct ggaggtggac etc

33

<210> 382

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 382

gaggtccacc tccaggagga ggtcgggtgcg cac

33

<210> 383

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 383

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccgc gcagctcgcc	300
ctcatcaagg agctgggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctggtctccg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccgc acaacctccc cgggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctcct cctggagggtg	780
gacctcgccc aggggcgggg gcccgaccgg gaggggctta gggccttcct ggagagggtg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggctg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcggtgccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg	1200
gagtgagcgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggcccac cccatcggtg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg ccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag	1920
gacatccaca ccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccagggt gcgggccttg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgcgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctccttg agggccccca agcgcgggcc	2400
gaggagggtg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgcc	2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 384

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 384

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Leu Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met

435	440	445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser		
450	455	460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg		
465	470	475
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg		
485	490	495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys		
500	505	510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu		
515	520	525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys		
530	535	540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg		
545	550	555
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly		
565	570	575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr		
580	585	590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp		
595	600	605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala		
610	615	620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys		
625	630	635
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu		
645	650	655
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly		
660	665	670
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile		
675	680	685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 385

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 385

ggggccttcg tgggctacgt cctctcccgc ccc

33

<210> 386

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 386

ggggcgggag aggacgtagc ccacgaaggc ccc

33

<210> 387

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 387

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcctg acaacctccc cgggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggctacg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca	1020

gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgagggg	ggggctagac	ctcgtgcccg	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgcgc	ccaccggggc	ctcctctcgg	agaggtcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcttgggcca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccccac	cccacgtggg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acggggccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccat	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggtca	ccaccaccac	2520
caccac						2526

<210> 388

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 388

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp

<400> 390
gttttctggc ttacctggt ccaggtgctt gaggaggttt tc 42

<210> 391

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 391
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccgc gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgagc 420
atcctcaccg ccgaccgga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagcacc tggaccaggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctggtgccc gggacgaccc catgctcctc 1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg 1200
gagtggacgg aggacgggc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320

ctctcccggg	tcctggccca	tatggaggcc	accgggggtac	ggcggggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaaggg	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgaccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catccccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcataagct	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaaggggtca	ccaccaccac	2520
caccac						2526

<210> 392

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 392

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
 210 215 220
 Asp Gln Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu

515					520					525					
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys
530						535					540				
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg
545					550					555					560
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly
				565					570						575
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr
			580					585					590		
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp
		595					600					605			
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
610					615					620					
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
625					630					635					640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 393

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 393
gagctctccc ggggtgcacac cgacctcccc ctg

33

<210> 394

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 394
caggggggagg tcggtgtgca cccgggagag etc

33

<210> 395

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 395

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc      420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcaca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca     1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctcggtgccc gggacgaccc catgctcctc     1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg     1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320
ctctccccgg tcctggccca tatggaggcc accgggttac ggcgggacgt ggcctacctt     1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc     1560
gcggtgctgg aggccctacg ggaggccccac cccatcgtgg agaagatcct ccagcaccgg     1620
```

gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacgggggag gcttagtagc 1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacact caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctctgg agggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 396

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 396

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

50					55					60					
Val 65	Phe	Val	Val	Phe	Asp 70	Ala	Lys	Ala	Pro	Ser 75	Phe	Arg	His	Glu	Ala 80
Tyr	Glu	Ala	Tyr	Lys 85	Ala	Gly	Arg	Ala	Pro 90	Thr	Pro	Glu	Asp	Phe 95	Pro
Arg	Gln	Leu	Ala 100	Leu	Ile	Lys	Glu	Leu 105	Val	Asp	Leu	Leu	Gly 110	Phe	Thr
Arg	Leu	Glu 115	Val	Pro	Gly	Tyr	Glu 120	Ala	Asp	Asp	Val	Leu 125	Ala	Thr	Leu
Ala	Lys 130	Lys	Ala	Glu	Lys	Glu 135	Gly	Tyr	Glu	Val	Arg 140	Ile	Leu	Thr	Ala
Asp 145	Arg	Asp	Leu	Tyr	Gln 150	Leu	Val	Ser	Asp	Arg 155	Val	Ala	Val	Leu	His 160
Pro	Glu	Gly	His	Leu 165	Ile	Thr	Pro	Glu	Trp 170	Leu	Trp	Glu	Lys	Tyr 175	Gly
Leu	Arg	Pro	Glu 180	Gln	Trp	Val	Asp	Phe 185	Arg	Ala	Leu	Val	Gly 190	Asp	Pro
Ser	Asp	Asn 195	Leu	Pro	Gly	Val	Lys 200	Gly	Ile	Gly	Glu	Lys 205	Thr	Ala	Leu
Lys 210	Leu	Leu	Lys	Glu	Trp	Gly 215	Ser	Leu	Glu	Asn	Leu 220	Leu	Lys	Asn	Leu
Asp 225	Arg	Val	Lys	Pro	Glu 230	Asn	Val	Arg	Glu	Lys 235	Ile	Lys	Ala	His	Leu 240
Glu	Asp	Leu	Arg	Leu 245	Ser	Leu	Glu	Leu	Ser 250	Arg	Val	His	Thr	Asp 255	Leu
Pro	Leu	Glu	Val 260	Asp	Leu	Ala	Gln	Gly 265	Arg	Glu	Pro	Asp	Arg	Glu	Gly 270
Leu	Arg	Ala 275	Phe	Leu	Glu	Arg	Leu 280	Glu	Phe	Gly	Ser	Leu 285	Leu	His	Glu
Phe 290	Gly	Leu	Leu	Glu	Ala	Pro 295	Ala	Pro	Leu	Glu	Glu 300	Ala	Pro	Trp	Pro

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro

	805		810		815										
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820					825					830		
Ser	Ala	Lys	Gly	His	His	His	His	His	His	His					
		835						840							

<210> 397
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 397
 gagctctccc ggggtgcacac cgacctctc ctg

33

<210> 398
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 398
 caggaggagg tcggtgtgca cccgggagag etc

33

<210> 399
 <211> 2526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 399

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccagagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcggcac cctggccaag aaggcggaaa aggaggggta cgagggtcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcaca ccgacctcct cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccc gggacgacct catgctcctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagg gtgaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgcgcc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgtc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcggcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggcccagag gatccgcgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860

cgcgctcctcg cccacctctc cggggacgaa aacctgatca gggctcttcca ggagggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgctcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgaact caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcacgc tcctccaggt cgccaacgag ctccctcctgg agggccccca agcgcgggcc 2400
 gaggagggtg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 400

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 400

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro

85							90							95						
Arg	Gln	Leu	Ala 100	Leu	Ile	Lys	Glu	Leu 105	Val	Asp	Leu	Leu	Gly 110	Phe	Thr					
Arg	Leu	Glu 115	Val	Pro	Gly	Tyr	Glu 120	Ala	Asp	Asp	Val	Leu 125	Ala	Thr	Leu					
Ala	Lys 130	Lys	Ala	Glu	Lys	Glu 135	Gly	Tyr	Glu	Val	Arg 140	Ile	Leu	Thr	Ala					
Asp 145	Arg	Asp	Leu	Tyr	Gln 150	Leu	Val	Ser	Asp	Arg 155	Val	Ala	Val	Leu	His 160					
Pro	Glu	Gly	His	Leu 165	Ile	Thr	Pro	Glu	Trp 170	Leu	Trp	Glu	Lys	Tyr 175	Gly					
Leu	Arg	Pro	Glu 180	Gln	Trp	Val	Asp	Phe 185	Arg	Ala	Leu	Val	Gly 190	Asp	Pro					
Ser	Asp	Asn 195	Leu	Pro	Gly	Val	Lys 200	Gly	Ile	Gly	Glu	Lys 205	Thr	Ala	Leu					
Lys	Leu 210	Leu	Lys	Glu	Trp	Gly 215	Ser	Leu	Glu	Asn	Leu 220	Leu	Lys	Asn	Leu					
Asp 225	Arg	Val	Lys	Pro	Glu 230	Asn	Val	Arg	Glu	Lys 235	Ile	Lys	Ala	His	Leu 240					
Glu	Asp	Leu	Arg	Leu 245	Ser	Leu	Glu	Leu	Ser 250	Arg	Val	His	Thr	Asp 255	Leu					
Leu	Leu	Glu	Val 260	Asp	Leu	Ala	Gln	Gly 265	Arg	Glu	Pro	Asp	Arg 270	Glu	Gly					
Leu	Arg	Ala 275	Phe	Leu	Glu	Arg	Leu 280	Glu	Phe	Gly	Ser	Leu 285	Leu	His	Glu					
Phe 290	Gly	Leu	Leu	Glu	Ala	Pro 295	Ala	Pro	Leu	Glu	Glu 300	Ala	Pro	Trp	Pro					
Pro 305	Pro	Glu	Gly	Ala	Phe 310	Val	Gly	Phe	Val	Leu 315	Ser	Arg	Pro	Glu	Pro 320					
Met	Trp	Ala	Glu	Leu 325	Lys	Ala	Leu	Ala 330	Ala	Cys	Arg	Gly	Gly	Arg 335	Val					

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly His His His His His His

835

840

<210> 401

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 401

```

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccc acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgga cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcccg acaacctccc cggggtaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca     1020
gacccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgctcctc     1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg     1200
gagtggacgg aggacccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc gtttggtct accacgaggt ggaaaagccc     1320

```

ctctcccggg	tcttgccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tgcaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaaggg	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgaccca	acctgcagaa	catccccgtc	cgcacccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgctccg	ggagatgggg	2340
gcccgcgatgc	tctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgcccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggt		2508

<210> 402

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 402

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu

20					25					30					
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65						70					75				80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145						150					155				160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225						230					235				240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Val Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu

770		775		780
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala				
785		790	795	800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro				
	805		810	815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu				
	820	825		830
Ser Ala Lys Gly				
	835			

<210> 403

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (19) .. (51)

<223> The bases in these positions are a synthesis of 91% base shown and 3% all other bases.

<400> 403	
ctccatcgga acctccttaa gcgcctcgag ggggaggaga agctcctttg gctctaccac	60
gaggtg	66

<210> 404

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 404

aaggaggttc cgatggag

18

<210> 405

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 405

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagag acttccccgc gcagctcgcc	300
ctcatcaagg agctgggtga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcggtcccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctctcg agaggctcca tcggaacctc	1260

```

cttaagcgcc tcgagggggt ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcgggccc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
gagcttaggc ttcccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccttacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg 1680
acgggcccgc tccacaccgc cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca ccagaccgc aagctggatg ttggcgctcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttggcgctcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgaact caacgcccgg 2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgcccacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctcgg agggccccca agcgcggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

```

<210> 406

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 406

```

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1           5           10          15

```

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Val Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu

515		520		525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys	530	535	540	
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg	545	550	555	560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly	565	570		
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr	580	585	590	
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp	595	600	605	
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala	610	615	620	
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys	625	630	635	640
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu	645	650	655	
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly	660	665	670	
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile	675	680	685	
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe	690	695	700	
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys	705	710	715	720
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp	725	730	735	
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala	740	745	750	
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala	755	760	765	

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly
835

<210> 407

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 407

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccagg acttccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcgga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840

gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcttgcccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgaggcg ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgaa acgaggggaa ggagaagctc ctttggtct accacgagggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttcccgccct gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag	1920
gacatccaca ccagaccgc aagctggatg ttggcgctcc ccccgaggc cgtggacccc	1980
ctgatgcgcc gggcgcccaa gacggtgaac ttggcgctcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctcgg agggccccca agcgcggggc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgcggtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt	2508

<210> 408

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Asn Glu Gly Lys Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys

705		710		715		720
Arg Gly Tyr Val	Glu Thr Leu Phe Gly	Arg Arg Arg Tyr Val	Pro Asp			
	725	730	735			
Leu Asn Ala Arg Val Lys Ser Val	Arg Glu Ala Ala Glu Arg	Met Ala				
	740	745	750			
Phe Asn Met Pro Val Gln Gly Thr	Ala Ala Asp Leu Met Lys Leu Ala					
	755	760	765			
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met	Gly Ala Arg Met Leu					
	770	775	780			
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala	Pro Gln Ala Arg Ala					
	785	790	795	800		
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met	Glu Lys Ala Tyr Pro					
	805	810	815			
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu						
	820	825	830			
Ser Ala Lys Gly						
	835					

<210> 409
 <211> 2508
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 409	
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgaggtccc cggctacgag	360

gcggacgacg	ttctcgccac	cctggccaag	aaggcgga	aggaggggta	cgaggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccagagggc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggggtgcga	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgct	tcgaggggga	ggagaagctc	ctttgcctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccaccgagg	1680
acgggcggcc	tcacacccc	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tcgaccccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggagggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggtctcccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaagt	gcgggccttg	atagaaaaga	ccctggagga	ggggagggaag	2160
cggggctacg	tggaaacctt	cttcggaaga	aggcgctacg	tgcccgacct	caacgccccg	2220

gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccggt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 410

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 410

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Phe Glu Gly Glu Glu Lys Leu Leu Cys
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu

	645		650		655
Ala Val Asp	Pro Leu Met Arg Arg	Ala Ala Lys Thr Val	Asn Phe Gly		
	660	665	670		
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile					
	675	680	685		
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe					
	690	695	700		
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys					
	705	710	715		720
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp					
	725	730		735	
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala					
	740	745		750	
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala					
	755	760		765	
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu					
	770	775		780	
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala					
	785	790		795	800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro					
	805		810		815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu					
	820		825		830
Ser Ala Lys Gly					
	835				

<210> 411

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 411

atgaattccg	aggcgatgct	tccgctcttt	gaacccaaag	gccgggtcct	cctgggtggac	60
ggccaccacc	tggcctaccg	caccttcttc	gccctgaagg	gcctcaccac	gagccggggc	120
gaaccggtgc	aggcggtcta	cggcttcgac	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaggccc	cctccttccg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgaggctcc	cggctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgaggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccgagggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cgggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgccgga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggaccttcc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccttttt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccccc	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctccc	caagcctcgt	ccacccgagg	1680
acgggccggc	tcacaccccc	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tggggccagag	gatccgccgg	1800

gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca ggggtcttcca ggagggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagt gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctcctcgg agggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 412

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro

85								90				95			
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Phe Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly

835

<210> 413

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (19)..(21)

<223> n is any base a,t,c, or g.

<400> 413

caggagctta ggcttcccn nttgaagaag acgaagaaga ca

42

<210> 414

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

cctaagctcg tcaaagag

18

<210> 415

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 415
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccc acccccagg acttccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgaggctcc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtcgc 420
atcctcaccg ccgaccgca cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccg ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gacccttg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttg cctcgaggga ggggctagac ctcgtgccc gggacgaccc catgctcctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc 1320
ctctcccggg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaaagggt gctctttgac 1500
gagcttaggc ttcccgtttt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860

cgcgctcctcg cccacctctc cggggacgaa aacctgatca gggctcttcca ggagggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgctcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 416

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 416

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Val Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp

595	600	605													
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
610						615					620				
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
625					630					635					640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
785					790					795					800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
			805						810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820					825					830		
Ser	Ala	Lys	Gly												
		835													

<210> 417

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 417

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctgggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc      420
atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttccgcgc cctcgtgggg gaccocctccg acaacctccc cgggggtcaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc      960
atgtgggagg agcttaaagc cctggccgcc tgcagggggc gccgcgtgca ccgggcagca     1020
gaccoccttg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccc gggacgaccc catgctcctc     1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggg ctacgggggg     1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggacctacct     1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440
```

```

ttggcggggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
gagcttaggc ttcccagttt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg 1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgaccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg ccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca ccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacgggtgaac ttcggcgtcc tctacggcat gtccgccccat 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacct caacgcccgg 2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcggggc 2400
gaggagggtg cggttttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggg 2508

```

<210> 418

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 418

```

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1           5           10          15

```

```

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20          25          30

```

```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly

```

35					40					45					
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
50						55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155				160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ser Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala

785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly
835

<210> 419

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 419

```
atgaattcgg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgga cctctacca ctctctccg accgcgtcgc cgtcctccac 480
cccaggggccc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctgcccc aggggcggga gcccagccgg gaggggctta gggccttcct ggagagggtg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
```

atgtggg	cg	agctt	aaagc	cctgg	ccgcc	tgcagg	ggcg	gccgc	gtgca	ccggg	cagca	1020																		
gaccc	cttgg	cg	ggg	gctaaa	ggac	ctcaag	gaggt	ccggg	gcct	cctcgc	caagg	acctc	1080																	
gccgt	cttgg	cctc	gag	gga	ggg	gctag	ac	ctcgt	gccc	ggg	acg	acc	catg	ctc	1140															
gcct	ac	ctc	tg	gg	ac	cttc	gaac	acc	acc	ccc	gag	ggg	gg	ctac	ggg	ggg	1200													
gagt	gg	ac	gg	ccgc	cc	acc	ggg	cc	ctc	ctc	tc	gg	ag	gg	ct	cca	tcg	ga	ac	ctc	1260									
ctta	ag	cg	cc	tcg	ag	ggg	gga	gg	aga	ag	ctc	cttt	gg	ct	ct	acc	ac	gag	gt	gg	aaa	ag	ccc	1320						
ctct	ccc	ggg	tc	ct	gg	cccc	tat	gg	ag	gg	cc	acc	ggg	gt	ac	gg	cg	gg	ac	gt	gg	c	ct	ac	ctt	1380				
cagg	cc	cttt	cc	ct	gg	ag	ct	tg	cg	gag	gag	at	cc	g	cc	gc	tc	cg	gg	ag	ga	gg	t	ct	tc	ccgc	1440			
ttgg	cg	ggg	cc	ac	cc	tt	caa	c	ct	ca	act	cc	cg	gg	ac	cag	tc	gg	aa	ag	gg	gt	g	ct	ctt	t	gac	1500		
gag	ct	tag	gc	tt	ccc	gc	ctt	ga	aga	ag	ac	g	a	ga	ag	ac	ag	g	ca	ag	cg	ctc	c	ac	cg	gt	g	cc	1560	
g	cg	gt	g	ct	gg	ag	gg	ac	cc	at	cg	tg	gg	ag	at	cc	tc	cc	ag	cg	ac	cg	gg	1620						
gag	ct	ca	cca	ag	ct	ca	aga	aa	ca	ct	ac	gt	g	ac	cc	ct	cc	ca	ag	cc	tc	gt	cc	ac	cc	g	ag	gg	1680	
ac	gg	g	cc	gc	cc	gc	tc	cc	ac	ac	cc	gc	ctt	ca	acc	ag	ac	gg	cc	ac	gg	g	ag	g	ct	tag	tag	ac	1740	
tcc	g	ac	cc	ca	ac	tc	g	ca	ga	aa	cat	ccc	gc	cg	ac	cc	cc	t	gg	g	cc	ag	ag	gat	cc	gc	cc	gg	1800	
gc	ctt	cg	tg	gg	cc	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	1860
cg	gc	tc	ct	cg	ccc	ac	ct	ctc	cg	ggg	ac	gaa	aac	ct	gat	ca	gg	gt	ctt	cca	gg	ag	ggg	g	aa	g	1920			
gac	at	cc	aca	ccc	ag	acc	gc	aag	ct	gg	at	g	tt	cg	gc	tc	ccc	g	g	ag	gc	cg	ct	cccc	1980					
ct	gat	gc	gc	ggg	cg	g	ccaa	gac	gg	t	ga	ac	tt	cg	gc	gc	tc	t	ct	ac	gg	cat	gt	cc	g	cc	cc	at	2040	
agg	ct	ct	ccc	agg	ag	ctt	gc	cat	ccc	ct	ac	gagg	gg	cg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	2100
tt	ccaa	ag	ct	tt	ccaa	ag	gt	gc	gg	gc	ct	gg	at	ag	aaa	aga	cc	ct	gg	ag	ga	gg	ggg	ag	ga	g	2160			
cg	ggg	g	ct	ac	tg	gaa	acc	ct	ct	cg	ga	aga	agg	cg	ct	ac	tg	ccc	g	ac	ct	ca	ac	g	ccc	cg	2220			
gt	ga	ag	ag	cg	tc	ag	gg	ag	gc	cg	gg	ag	cg	at	gg	cc	tt	ca	ac	at	g	ccc	gt	cc	ag	gg	g	acc	2280	
g	cc	g	cc	g	acc	tc	at	ga	ag	ct	gc	cat	gg	tg	aag	ct	ctt	cc	ccc	g	ct	cc	g	gg	ag	at	g	ggg	2340	
g	ccc	g	cat	gc	tc	ct	cc	ag	gt	cg	cca	ac	gag	ct	ct	ct	ct	gg	ag	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	2400
gag	g	ag	gt	gg	cg	g	ctt	t	gg	c	ca	ag	g	gg	cc	at	gg	g	ag	g	gg	gg	gg	gg	gg	gg	gg	gg	gg	2460
ct	g	g	ag	gt	gg	ag	gt	gg	gg	g	ag	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	2508

<210> 420

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 420

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Gly Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 422

ggtggagcgc ttgcc

15

<210> 423

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 423

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcgga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020

gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgagggg	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagagggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgcccc	ccaccggggc	ctcctctcgg	agaggtcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcttgcccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcgaggagg	atccgccccg	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagctta	1560
gcggtgctgg	aggccctacg	ggaggccccac	cccacgtggg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acgggccccg	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgcccc	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccccgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catccccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgccccg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatccccct	cgcggtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggt		2508

<210> 424

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 424

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg

485										490					495				
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys				
			500					505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Leu	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535					540								
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
545					550					555					560				
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
				565					570						575				
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
			580					585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
	610					615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
625					630					635					640				
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
				645					650					655					
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly				
			660					665					670						
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile				
		675					680					685							
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe				
	690					695					700								
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys				
705					710					715					720				
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp				
				725					730					735					

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly
835

<210> 425

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> n

<222> (19)..(21)

<223> n is any base a,t,c, or g.

<220>

<221> misc_feature

<222> (19)..(21)

<223> n is any base a,t,c, or g.

<400> 425
ggcaagcgct ccaccagcnn ngcgggtgctg gagggccctac gg 42

<210> 426

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 426
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctgggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcggtggg gacccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtggggcg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctcggtgccc gggacgaccc catgctcctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg 1200
gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagggt ggaaaagccc 1320

ctctcccggtg tcttgcccca tatggaggcc accgggggtac ggcggggacgt ggccctacctt 1380
 caggcccttt ccttgagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
 ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
 gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagccgt 1560
 gcggtgctgg aggccttacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
 gagctacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg 1680
 acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
 tccgaccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
 gccttcgtgg ccgaggcggtg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
 cgcgctctcg cccacctctc cggggacgaa aacctgatca gggctcttcca ggaggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcgcccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggg 2508

<210> 427

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 427

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu

20					25					30					
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
	35						40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65						70					75				80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145						150					155				160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225						230					235				240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Arg Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu

770		775		780
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala				
785		790		795
				800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro				
	805		810	815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu				
	820		825	830
Ser Ala Lys Gly				
	835			

<210> 428

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840

agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
aaagccctca	gggacctgaa	ggaggcgccg	gggcttctcg	ccaaagacct	gagcgttctg	1080
gccctgaggg	aaggccttgg	cctcccgcgc	ggcgacgacc	ccatgctcct	cgccctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggccccgc	gctacggcgg	ggagtggacg	1200
gaggaggcgg	gggagcgggc	cgccctttcc	gagaggctct	tgcceaacct	gcttaagagg	1260
cttgaggggg	aggagaggct	cctttggctt	taccgggagg	tggagaggcc	cctttccgct	1320
gtcctggccc	atatggaggc	cacgggggtg	cgccgggacg	tggcctatct	cagggccttg	1380
tccctggagg	tggccgagga	gatcgcccg	ctcgaggccg	aggtcttccg	cctggccggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagctaggg	1500
cttcccgcga	tcaagaagac	gcaaaagacc	ggcaagcgct	ccaccagcgc	cgccgtcctg	1560
gaggccctcc	gcgaggccca	ccccatcgtg	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctgaaga	gcacctacat	tgaccccttg	ccggacctca	tccaccccag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgccg	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	caggggtgctg	1860
gcccacctct	ccggcgacga	gaacctgatc	cggggtcttc	aggagggggc	ggacatccac	1920
acggagaccg	ccagctggat	gttcggcgtc	ccccgggagg	ccgtggaccc	cctgatgcgc	1980
cgggcgccca	agaccatcaa	cttcggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	ccgcgcctac	gtgccagacc	tagaggcccc	ggtgaagagc	2220
gtgcgggagg	cggccgagcg	catggccttc	aacatgcccc	tccaggggcac	cgccgcccgc	2280
ctcatgaagc	tggctatgg	gaagctcttc	cccaggctgg	aggaaatggg	ggccaggatg	2340
ctccttcagg	tgcceaacga	gctggctctc	gaggccccaa	aagagagggc	ggaggccctg	2400
gcccggctgg	ccaaggaggt	catggagggg	gtgtatcccc	tggccgtgcc	cctggagggtg	2460
gaggtgggga	taggggagga	ctggctctcc	gccaaggag			2499

<210> 429

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr

705		710		715		720									
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val
785					790					795					800
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val
			805						810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		

Glu

<210> 430
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 430
 acgggggtgc gccgggacgt ggcctat

27

<210> 431
 <211> 2508
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctacca ctctctccg accgcgtcgc cgtcctccac	480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg	1200
gagtggacgg aggacggcg ccaccgggccc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagggt ggaaaagccc	1320
ctctccccgg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgcccgc tcgaggagga ggtcttccgc	1440
ttggcgggccc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttcccaagtt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccttacg ggaggccccc cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccctccc caagcctcgt ccaccgagg	1680
acgggccgcc tcacacccc cttcaaccag acggccacgg ccacggggag gcttagtagc	1740

tccgacccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgccgg 1800
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagg gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaacct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccagggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 432

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr

580																585																590															
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp																																
		595					600					605																																			
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala																																
		610					615					620																																			
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys																																
		625					630					635																																			
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu																																
				645							650			655																																	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly																																
				660							665			670																																	
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile																																
				675							680			685																																	
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe																																
				690							695			700																																	
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys																																
				705							710			715			720																														
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp																																
				725							730			735																																	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala																																
				740							745			750																																	
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala																																
				755							760			765																																	
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu																																
				770							775			780																																	
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala																																
				785							790			795			800																														
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro																																
				805							810			815																																	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu																																
				820							825			830																																	

Ser Ala Lys Gly
835

<210> 433

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433

cttaggcttc ccaagttgaa gaagacgaag aagaca

36

<210> 434

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 434

tgtctttcttc gtctttcttca acttggaag cctaag

36

<210> 435

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 435

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac

60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc

240

tacgaggcct	acaaggcggg	gagggccccc	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgaggtccc	cggtctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgaggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccagggggc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggtgcgca	ccgacctccc	cctggaggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcggga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagagggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatcgcca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catccccctac	gaggaggcgg	tggcctttat	agagcgctac	2100

ttccaaagct tccccaaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcgaaga aggcgctacg tgcccgcacct caacgcccgg 2220
 gtgaagagcg tcaggaggcg cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gccgcacatgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcggggc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 436

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys

625		630		635		640									
Asp	Ile	Ala	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
785					790					795					800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
				805					810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820					825					830		
Ser	Ala	Lys	Gly												
			835												

<210> 437

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437

gaggggaagg acatcgccac ccagaccgca agc

33

<210> 438

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 438

gcttgcggtc tgggtggcga tgtccttccc etc

33

<210> 439

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 439

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120

gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg ccgtcttctg ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240

tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc 420

atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac 480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540

cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag 600

ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagagggtg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	ccccgcctcc	cctggaggag	900
gccccctggc	ccccgccgga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtggggcg	agcttaaagc	cctggccgcc	tgcagggggc	gccgcgtgca	ccgggcagca	1020
gacccttggt	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtgagcgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagccg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccccc	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctccc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacaccgc	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tcgaccccca	acctgcagaa	catccccgtc	cgcacccctt	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggagggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggagggaag	2160
cggggctacg	tggaaacctt	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	agggccccca	agcgcgggcc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcggtgccc	2460

ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt

2508

<210> 440

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Pro Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile

675	680	685
Pro Tyr Glu Glu Ala Val	Ala Phe Ile Glu Arg	Tyr Phe Gln Ser Phe
690	695	700
Pro Lys Val Arg Ala Trp	Ile Glu Lys Thr	Leu Glu Glu Gly Arg Lys
705	710	715
Arg Gly Tyr Val	Glu Thr Leu Phe Gly	Arg Arg Arg Tyr Val
	725	730
Leu Asn Ala Arg	Val Lys Ser Val	Arg Glu Ala Ala Glu
	740	745
Phe Asn Met Pro	Val Gln Gly Thr	Ala Ala Asp Leu
	755	760
Met Val Lys Leu	Phe Pro Arg Leu	Arg Glu Met Gly
	770	775
Leu Gln Val Ala	Asn Glu Leu Leu Leu	Glu Ala Pro Gln Ala
	790	795
Glu Glu Val Ala	Ala Leu Ala Lys Glu	Ala Met Glu Lys Ala
	805	810
Leu Ala Val Pro	Leu Glu Val Glu	Val Gly Met Gly
	820	825
Ser Ala Lys Gly		Glu Asp Trp Leu
	835	830

<210> 441

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 441

cccgccttga agaagccgaa gaagacaggc aag

<210> 442

33

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 442

cttgctgtc ttcttcggct tcttcaaggc ggg

33

<210> 443

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tcacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttgcc	840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960

gatctttctgg	ccctggccgc	cgccaggggc	ggccgcgttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcggtgctg	1080
gccctgaggg	aagggattgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggatcctt	ccaacaccgc	ccccgaaggg	gtagcccggc	gctacggggg	ggagtggacc	1200
gaggagggcg	gggaaagggc	gctgctttcc	gaaaggcttt	acgccgccct	cctgaagcgg	1260
cttaaggggg	aggagaggct	tctttggctt	tacgaggagg	tggaaaagcc	cctttcgcgg	1320
gtcctggccc	acatggaggc	cacgggggta	cggttgatg	tggcctactt	aaaggccctt	1380
tccctggagg	tggaggcgga	gataaggcgc	ttcgaggagg	aggtccaccg	cctggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcatccttga	cgagcttggg	1500
cttcccccca	tcaagaagac	gaggaagacg	ggcaagcgct	ccaccagcgc	cgccgttttg	1560
gaggccttgc	gggaggctca	tcccatcggt	gaccgcatcc	ttcagtaccg	ggagctttcc	1620
aagctcaagg	gaacctacat	cgatcccttg	cctgccctgg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatcct	1740
aatctgcaaa	atatccccgt	gcgcaccctt	ttggggccagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctaatc	cggtcttcc	aggagggcca	ggacatccac	1920
accagacgg	ccagctggat	gttcggcggt	ccccagagg	ccgtggattc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggcgct	ctctacggca	tgtccgcca	ccggctttcg	2040
ggagagctgg	ccatccccta	cgaggaggcg	gtggccttca	tcgagcggta	tttccagagc	2100
tacccaagg	tgcgggcctg	gattgagaaa	accctggcgg	aaggacggga	acggggctat	2160
gtggaaaccc	tctttggccg	ccggcgctac	gtgcccgaact	tggcttcccc	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgcagg	tgcacaacga	actggtcctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaaggtgcc	cttggagggtg	2460
gaagtgggca	tcggggagga	ctggctttcc	gccaaggcc			2499

<210> 444

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val Tyr Arg Ala
 325 330 335
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu
 355 360 365
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala
 405 410 415
 Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val
 450 455 460
 Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val
595 600 605

Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His
625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
645 650 655

Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser

	725		730		735
Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	740		745		750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	755		760		765
Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val	770		775		780
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val	785		790		795
Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val	805		810		815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	820		825		830

Ala

<210> 445

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcagagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480

gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccgggggt	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcg	accgacctgc	ccctggagggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
ccccgcggg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcaac	aagcccgggt	1020
gaggccctgg	ccgacctcaa	ggaggcccgg	gggttcctgg	ccaaggacct	ggccgttttg	1080
gccctgcggg	agggggtggc	cctggacccc	acggacgacc	ccctcctgggt	ggcctacctc	1140
ctggacccgg	ccaacaccca	ccccgagggg	gtggcccggc	gctacggggg	cgagttcacg	1200
gaggacgcag	cggagagggc	cctcctctcc	gagaggctct	tccagaacct	ctttaaacgg	1260
ctttccgaga	agctcctctg	gctctaccag	gaggtggagc	ggccccctctc	ccgggtcttg	1320
gcccacatgg	aggcccgggg	ggtgaggctg	gacgtccccc	ttctggaggc	cctctccttt	1380
gagctggaga	aggagatgga	gcgcctggag	ggggagggtct	tccgtttggc	cggccacccc	1440
ttcaacctca	actcccgcga	ccagctggaa	agggctcctct	ttgacgagct	gggcctcacc	1500
ccggtgaagc	ggacgaagaa	gacgggcaag	cgctccaccg	cccagggggc	cctggaggcc	1560
ctccgggggg	cccaccccat	cgtggagctc	atcctccagt	accgggagct	ttccaagctc	1620
aaaagcacct	acctggaccc	cctgccccgg	ctcgctccacc	cgcggaaggc	ccggctccac	1680
accgcgttca	accagacggc	cacggccaag	ggaaggcttt	ccagctccga	ccccaacctg	1740
cagaacatcc	ccgtgcgcac	ccccttgggg	cagcgcatcc	gcaaggcctt	cgtggccgag	1800
gaggggtggc	tccttttggc	ggcggaactac	tcccagattg	agctccgggt	cctggcccac	1860
ctctcggggg	acgagaacct	gaagcgggtc	ttccgggagg	ggaaggacat	ccataccgag	1920
accgccgcct	ggatgttcgg	cttagacccc	gctctggtgg	atccaaagat	gcgccggggc	1980
gccaagacgg	tcaacttcgg	cgtcctctac	gggatgtccg	cccacaggct	ctcccaggag	2040
ctcggcatag	actacaagga	ggcggaggcc	tttattgagc	gctacttcca	gagcttcccc	2100
aaggtgcggg	cctggataga	aaggaccctg	gaggagggcc	ggacgcgggg	ctacgtggag	2160
acctgttcg	gcaggaggcg	ctatgtgcc	gacctggcct	cccgggtccg	ctcggtgcgg	2220
gaggcggcgg	agcggatggc	cttcaacatg	cccgtgcagg	gcaccgccgc	cgacctgatg	2280
aagatcgcca	tggtcaagct	cttccccagg	ctaaagcccc	tgggggcccc	cctcctcctc	2340

caagtggcca acgagctggt cctggagggtg cccgaggacc gggccgagga ggccaaggcc 2400
ctggtcaagg aggtcatgga gaacgcctac cccctggacg tgcccctcga ggtggagggtg 2460
ggcgtgggtc gggactggct ggaggcgaag caggat 2496

<210> 446

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly Phe
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala Leu
 355 360 365

Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro Ala
 370 375 380

Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe Thr
 385 390 395 400

Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln Asn
 405 410 415

Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu Val
 420 425 430

Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly Val
 435 440 445

Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu Lys
 450 455 460

Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495

Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly Lys Arg Ser
 500 505 510

Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile Val
 515 520 525

Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr Tyr
 530 535 540

Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu His
 545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590

Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala Ala
 595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620

Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu
 625 630 635 640

Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro Lys
 645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met

660	665	670
Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu Ala		
675	680	685
Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala		
690	695	700
Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val Glu		
705	710	715
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val		
725	730	735
Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val		
740	745	750
Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu Phe		
755	760	765
Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val Ala Asn		
770	775	780
Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys Ala		
785	790	795
Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro Leu		
805	810	815
Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln Asp		
820	825	830

<210> 447

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 447

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120

gaaccggtgc	aggcggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	cgtcttcgt	ggtctttgac	gccaaaggccc	cctccttccg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgagggtccc	cggctacgag	360
gcggaacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgagggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgtcctccac	480
cccgaaggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cgggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaaccg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgccgga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgttta	ccgggcggag	1020
gatcccttgg	aggccttgcg	ggggcttggg	gaggtgaggg	ggcttttggc	caaggacctg	1080
gcggtgctgg	ccctgagggg	agggattgcc	ctggcaccgg	gcgacgaccc	catgctcctc	1140
gcctacctcc	tggatccttc	caacaccgcc	cccgaagggg	tagcccggcg	ctacgggggg	1200
gagtggaccg	aggaggcggg	ggaaagggcg	ctgctttccg	aaaggcttta	cgccgccctc	1260
ctgaagcggc	ttaaggggga	ggagaggctt	ctttggcttt	acgaggaggt	ggaaaagccc	1320
ctttcgcggg	tcctggccca	catggaggcc	acgggggtac	ggttggatgt	ggcctactta	1380
aaggcccttt	ccctggagggt	ggaggcggag	ataaggcgct	tcgaggagga	ggtccaccgc	1440
ctggccgggc	atcctttcaa	cctgaactcc	cgggaccagc	tggaaagggg	catctttgac	1500
gagcttgggc	ttcccgccat	caagaagacg	aggaagacgg	gcaagcgctc	caccagcgcc	1560
gccgttttgg	aggccttgcg	ggaggctcat	cccatcgtgg	accgcaccc	tcagtaccgg	1620
gagctttcca	agctcaaggg	aacctacatc	gatcccttgc	ctgccctggg	ccaccccaag	1680
acgaaccgcc	tccacacccg	tttcaaccag	acggccaccg	ccacggggag	gcttagcagc	1740
tcggatccta	atctgcaaaa	tatccccgtg	cgcacccctt	tgggccagcg	gatccgccgg	1800
gccttcgtgg	ccgaggaggg	gtggaggctg	gtgggtttgg	actacagcca	gattgagctc	1860
agggtcctgg	cgcacctttc	cggggacgag	aacctaatcc	gggtcttcca	ggagggccag	1920
gacatccaca	cccagacggc	cagctggatg	ttcggcgtgc	ccccagaggc	cgtggattcc	1980

ctgatgcgcc gggcggccaa gaccatcaac ttcggcgtcc tctacggcat gtccgcccac 2040
 cggctttcgg gagagctggc catcccctac gaggaggcgg tggccttcat cgagcgggat 2100
 ttccagagct accccaaggt gcgggcctgg attgagaaaa ccttggcgga aggacgggaa 2160
 cggggctatg tggaaaccct ctttggccgc cggcgctacg tgcccgaact ggcttcccgg 2220
 gtgaagagca tccgggaggc agcggagcgc atggccttca acatgccggg ccagggggacc 2280
 gccgcggatt tgatgaaact ggccatggtg aagctctttc ccaggcttca ggagctgggg 2340
 gccaggatgc ttttgcaggt gcacaacgaa ctggtcctcg aggtcccaa ggagcaagcg 2400
 gaggaagtcg cccaggaggc caagcggacc atggaggagg tgtggccctt gaagggtgcc 2460
 ttggaggtgg aagtgggcat cggggaggac tggctttccg ccaaggcc 2508

<210> 448

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 448

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

Tyr Arg Ala Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365

Ile Ala Leu Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

Tyr Ala Ala Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp
 420 425 430

Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser
 450 455 460

Leu Glu Val Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Ile Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys
 530 535 540

Leu Lys Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys
 545 550 555 560

Thr Asn Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp
 595 600 605

Arg Leu Val Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala

610	615	620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln 625 630 635 640		
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu 645 650 655		
Ala Val Asp Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly 660 665 670		
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile 675 680 685		
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr 690 695 700		
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu 705 710 715 720		
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp 725 730 735		
Leu Ala Ser Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala 740 745 750		
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala 755 760 765		
Met Val Lys Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu 770 775 780		
Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala 785 790 795 800		
Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro 805 810 815		
Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu 820 825 830		
Ser Ala Lys Ala 835		

<210> 449

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 449

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcg accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac ccgagagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtcca ccgggcaaca     1020
agcccggttg aggccttggc cgacctcaag gaggccggg ggttcctggc caaggacctg     1080
gccgttttgg ccctgcggga ggggggtggc ctggaccca cgacgaccc cctcctggtg     1140
gcctacctcc tggacccggc caacaccac cccgaggggg tggcccggcg ctacgggggc     1200
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc     1260
tttaaacggc tttccgagaa gtcctcttgg ctctaccagg aggtggagcg gcccctctcc     1320
cgggtcttgg ccacatgga ggcccggggg gtgaggctgg acgtccccct tctggaggcc     1380
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc     1440
ggccaccctc tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg     1500
ggcctcaccg cggtgaagcg gacgaagaag acgggcaagc gctccaccgc ccagggggcc     1560
```

ctggaggccc tccggggggc ccaccccatc gtggagctca tcctccagta ccgggagctt 1620
 tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccaccc gcggacgggc 1680
 cggtccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac 1740
 cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc 1800
 gtggccgagg aggggtggct ccttttggcg gcggactact ccagattga gctccgggtc 1860
 ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc 1920
 cataccgaga ccgccgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg 1980
 cgccgggcgg ccaagacggc caacttcggc gtcctctacg ggatgtccgc ccacaggctc 2040
 tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag 2100
 agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc 2160
 tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc ccgggtccgc 2220
 tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac 2340
 ctctctctcc aagtggccaa cgagctggtc ctggagggtg ccgaggaccg ggccgaggag 2400
 gccaaagccc tgggtcaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag 2460
 gtggagggtg gcgtgggtcg ggactggctg gaggcgaagc aggat 2505

<210> 450

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 450

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	

Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		

Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

50	55	60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala 65 70 75 80		
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro 85 90 95		
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr 100 105 110		
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu 115 120 125		
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala 130 135 140		
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His 145 150 155 160		
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly 165 170 175		
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro 180 185 190		
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu 195 200 205		
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu 210 215 220		
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu 225 230 235 240		
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu 245 250 255		
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly 260 265 270		
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu 275 280 285		
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro 290 295 300		

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350
 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
 770 775 780

Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu
 785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp

	805	810	815	
Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala				
	820	825	830	
Lys Gln Asp				
	835			
<210>	451			
<211>	24			
<212>	DNA			
<213>	Artificial Sequence			
<220>				
<223>	Synthetic			
<400>	451			
cttctctcat ccgccaaaac agcc				24
<210>	452			
<211>	2526			
<212>	DNA			
<213>	Artificial Sequence			
<220>				
<223>	Synthetic			
<400>	452			
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac				60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc				120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac				180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc				240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc				300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggctacgag				360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtcgc				420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac				480
cccgagggcc acctcatcac cccggagtgg ctttggggaga agtacggcct caggccggag				540

cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcgggg	gccccgaccg	gaggggctta	gggccttcct	ggagagggtg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggagg	agcttaaagc	cctggccgcc	tgcaggggag	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccaccgagg	1680
acgggcccgc	tccacaccgc	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcaccccct	tgggcccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggagggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaagggt	gcgggccttg	atagaaaaga	ccctggagga	ggggagggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgcccagc	tcataagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccagggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400

gaggaggtgg	cggttttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaaggggtca	ccaccaccac	2520
caccac						2526

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 453

ctcctccacg agttcggc

18

<210> 454

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 454

atgaattccc	tgccccctctt	tgagcccaag	ggccgggtgc	ttctggtgga	cggccaccac	60
ctggcctacc	gtaccttttt	tgccctgaag	ggcctcacca	ccagccgcgg	ggagccggtc	120
caggcgggtg	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
gtgatcgtgg	tgtttgacgc	caaggccccc	tccttccgcc	accagacctt	cgaggcctac	240
aaggcggggc	gggctcccac	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggctt	taccgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gaaggctacg	aagtgcgcac	cctcaccgcg	420
gaccgggacc	tttaccagct	tctttcggag	cgaatctcca	tccttcaccc	ggaggggttac	480
ctgatcacc	cggagtggct	ttgggagaag	tatgggctta	agccttccca	gtgggtggac	540
taccgggcct	tggccgggga	cccttccgac	aacatccccg	gcgtgaaggg	catcggggag	600
aagacggcgg	ccaagctgat	ccgggagtgg	ggaagcctgg	aaaaccttct	taagcacctg	660

gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720
ctatccctgg agctatcccc ggtgcacacg gacttgctcc ttcaggtgga cttcgccccg	780
cgccgggagc cggaccggga ggggcttaag gccttttttg agaggctgga gttcggaagc	840
ctcctccacg agttcggcct gttggaaaag ccggtggcgg cggaggaagc tccctggccg	900
ccccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag	960
cttaacgcct tggccgcgc ctggggcggc cgcgtgcacc gggcagcaga ccccttggcg	1020
gggctaaagg acctcaagga ggtccggggc ctcctcgcca aggacctcgc cgtcttggcc	1080
tcgagggagg ggctagacct cgtgccccgg gacgacccca tgctcctcgc ctacctctg	1140
gacctttcga acaccacccc cgaggggggtg gcgcggcgct acggggggga gtggacggag	1200
gacgccgccc accgggccct cctctcggag aggctccatc ggaacctcct taagcgcctc	1260
gagggggagg agaagctcct ttggctctac cagcaggtgg aaaagcccct ctcccgggtc	1320
ctggcccata tggaggccac cgggggtacgg cgggacgtgg cctaccttca ggccctttcc	1380
ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttccgctt ggccggccac	1440
cccttcaacc tcaactcccc ggaccagctg gaaaggggtg tctttgacga gcttaggctt	1500
ccgccttga agaagacgaa gaagacaggc aagcgctcca ccagcgccgc ggtgctggag	1560
gccctacggg aggcccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag	1620
ctcaagaaca cctacgtgga cccctccca agcctcgctc acccgaggac gggccgcctc	1680
cacaccgcgt tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac	1740
ctgcagaaca tccccgtccg ccccccttg ggccagagga tccgccgggc cttcgtggcc	1800
gaggcggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgctcctgcc	1860
cacctctccg gggacgaaaa cctgatcagg gtcttccagg aggggaagga catccacacc	1920
cagaccgcaa gctggatgtt cggcgtcccc ccggaggccg tggaccccct gatgcgccg	1980
gcggccaaga cggatgaactt cggcgtcctc tacggcatgt ccgcccatag gctctcccag	2040
gagcttgcca tccccctacga ggaggcgggt gcctttatag agcgctactt ccaaagcttc	2100
cccaagggtg gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg	2160
gaaaccctct tcggaagaag gcgctacgtg ccgacctca acgcccgggt gaagagcgtc	2220
agggaggccg cggagcgcac ggccttcaac atgcccgtcc agggcaccgc cgccgacctc	2280
atgaagctcg ccatggtgaa gctcttcccc cgctccggg agatgggggc ccgcatgctc	2340
ctccaggctg ccaacgagct cctcctggag gcccccaag cgcgggccga ggaggtggcg	2400
gctttggcca aggaggccat ggagaaggcc tatccccctg ccgtgcccct ggaggtggag	2460
gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac	2514

<210> 455

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 455

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctgggtga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc      420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac      480
cccgaggggc acctcatcac cccggagtgg ctttgggaga agtatgggct taagccttcc      540
cagtgggtgg actaccgggc cttggccggg gacccttccg acaacatccc cggcgtgaag      600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt      660
cttaagcacc tggaacaggt gaaacctgcc tccgtgcggg agaagatcct tagccacatg      720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcagggtg      780
gacttcgccc ggcgccggga gccggaccgg gaggggctta aggccttttt ggagaggctg      840
gagttcggaa gcctcctcca cgagttcggc ctgttggaag gcccggtggc ggcggaggaa      900
gctccctggc cgccccccga gggagccttc gtgggggtacg ttctttcccg ccccgagccc      960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca     1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctcggtccccg gggacgaccc catgctcctc     1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg     1200
gagtggacgg aggacgccgc ccaccgggcc ctccctctcg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtctt accacgaggt ggaaaagccc     1320
ctctcccggg tcttggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt     1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc     1440
```

```

ttggcggggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccttacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg 1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgccccat 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcct caacgcccgg 2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgcccacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctcgtg agggccccca agcgcggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

```

<210> 456

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 456

```

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1           5           10          15

```

```

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
          20          25          30

```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro
 180 185 190
 Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala
 195 200 205
 Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
 210 215 220
 Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
 225 230 235 240
 Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
 245 250 255
 Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Trp Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys

- 704 -

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 457

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 457

ttccaggtgc ttgaggaggt tttccag

27

<210> 458

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 458

ctcctcaagc acctggaaca ggtgaaa

27

<210> 459

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 459

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctacca ctcgtctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagcacc tggaacaggt gaaacctgcc tccgtgcggg agaagatcct tagccacatg	720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcagggtg	780
gacttcgccc ggcgcgggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcggaa gcctcctcca cgagttcggc ctgttgga aa gcccggtggc ggcggaggaa	900
gctccctggc cgcgcgcga gggagccttc gtggggtacg ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttg cctcgaggga ggggctagac ctcgtgcccg gggacgacct catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgcgcgc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gaccctcc caagcctcgt ccaccgagg	1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740

tccgacccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgccgg 1800
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgccccat 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaacctt cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc ccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt cgccaacgag ctctccttg agggccccca agcgcggggc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 460

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 460

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala

65		70		75		80									
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu
	210					215					220				
Glu	Gln	Val	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met
225					230					235					240
Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu
				245					250					255	
Leu	Leu	Gln	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu

	820	825	830
Ser Ala Lys Gly His His His His His His			
	835	840	
<210>	461		
<211>	27		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	461		
gtccagggttc ttgaggaggt tttccag			27
<210>	462		
<211>	27		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	462		
ctcctcaaga acctggaccg ggtaaag			27
<210>	463		
<211>	2532		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	463		
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac			60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc			120

gaaccgggtgc	aggcgggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcatcgt	ggtctttgac	gccgaggccc	cctccttccg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcc	tcgaggctcc	cggctacgag	360
gcgagacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgagggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccgagggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gaccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccggac	tcgctccggc	gcaagataga	ggcgcacctc	720
gaggacctcc	acctctcctt	agacctggcc	cgcacccgca	ccgacctccc	cctggagggtg	780
gactttaagg	ccctgcgccg	caggaccccc	gacctggagg	gcctgagggc	ctttttggag	840
gagctggagt	tcggaagcct	cctccacgag	ttcggcctcc	tgggagggga	gaagccccgg	900
gaggaggccc	cctggcccc	gcccgaagg	gccttcgtgg	gcttcctcct	ttcccgaag	960
gagcccatgt	gggcggagct	tctggccctg	gcggcggcct	cgggcggccg	cgtgcaccgg	1020
gcagcagacc	ccttggcggg	gctaaaggac	ctcaaggagg	tccggggcct	cctcgccaag	1080
gacctgcgcg	tcttggcctc	gagggagggg	ctagacctcg	tgcccgggga	cgaccccatg	1140
ctcctcgcc	acctcctgga	cccttcgaac	accacccccg	agggggtggc	gcggcgctac	1200
gggggggagt	ggacggagga	cgccgccac	cgggccctcc	tctcgagag	gctccatcgg	1260
aacctcctta	agcgccctga	gggggaggag	aagctccttt	ggctctacca	cgagggtggaa	1320
aagccccctct	cccgggtcct	ggcccatatg	gaggccaccg	gggtacggcg	ggacgtggcc	1380
taccttcagg	ccctttccct	ggagcttgcg	gaggagatcc	gccgcctcga	ggaggaggtc	1440
ttccgcttgg	cgggccaccc	cttcaacctc	aactcccggg	accagctgga	aaggggtgctc	1500
tttgacgagc	ttaggcttcc	cgccttgaag	aagacgaaga	agacaggcaa	gcgctccacc	1560
agcgccgcgg	tgctggaggc	cctacgggag	gcccaccca	tcgtggagaa	gatcctccag	1620
caccgggagc	tcaccaagct	caagaacacc	tacgtggacc	ccctcccaag	cctcgtccac	1680
ccgaggacgg	gccgcctcca	caccgccttc	aaccagacgg	ccacggccac	ggggaggcctt	1740
agtagctccg	accccaacct	gcagaacatc	cccgtccgca	cccccttggg	ccagaggatc	1800
cgcggggcct	tcgtggccga	ggcgggttgg	gcgttggtgg	ccctggacta	tagccagata	1860
gagctccgcg	tcctcgccca	cctctccggg	gacgaaaacc	tgatcagggt	cttccaggag	1920
gggaaggaca	tccacacca	gaccgcaagc	tggatgttcg	gcgtcccccc	ggaggccgtg	1980

gacccccctga tgcgcggggc ggccaagacg gtgaacttcg gcgtcctcta cggcatgtcc 2040
gccccataggc tctcccagga gcttgccatc cctacgagg aggcgggtggc ctttatagag 2100
cgctacttcc aaagcttccc caaggtgcgg gcctggatag aaaagaccct ggaggagggg 2160
aggaagcggg gctacgtgga aaccctcttc ggaagaaggc gctacgtgcc cgacctcaac 2220
gccccgggtga agagcgtcag ggaggccgcg gagcgcacatg ccttcaacat gcccgccag 2280
ggcaccgcgc cgcacctcat gaagctcgcc atggtgaagc tttccccccg cctccgggag 2340
atggggggccc gcatgctcct ccaggctcgcc aacgagctcc tcctggaggc cccccaagcg 2400
cgggcccagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
gtgccccctgg aggtggagggt ggggatgggg gaggactggc tttccgcca gggtcaccac 2520
caccaccacc ac 2532

<210> 464

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 464

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr

100					105					110					
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
	115						120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Asp	Ser	Leu	Arg	Arg	Lys	Ile	Glu	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	His	Leu	Ser	Leu	Asp	Leu	Ala	Arg	Ile	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Phe	Lys	Ala	Leu	Arg	Arg	Arg	Thr	Pro	Asp	Leu
			260					265					270		
Glu	Gly	Leu	Arg	Ala	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Gly	Ser	Leu	Leu
		275					280					285			
His	Glu	Phe	Gly	Leu	Leu	Gly	Gly	Glu	Lys	Pro	Arg	Glu	Glu	Ala	Pro
	290					295					300				
Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu	Ser	Arg	Lys
305					310					315					320
Glu	Pro	Met	Trp	Ala	Glu	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Ser	Gly	Gly
				325					330					335	
Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys
			340					345					350		

Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365

Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380

Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400

Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415

Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445

His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460

Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480

Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495

Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510

Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525

Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540

Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560

Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575

Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590

Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605

Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro
 645 650 655
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn
 660 665 670
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu
 675 680 685
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln
 690 695 700
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly
 705 710 715 720
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val
 725 730 735
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg
 740 745 750
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys
 755 760 765
 Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg
 770 775 780
 Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala
 785 790 795 800
 Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala
 805 810 815
 Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp
 820 825 830
 Trp Leu Ser Ala Lys Gly His His His His His His
 835 840

<210> 465

<211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 465
 gacgtccttc ggggtgatga ggtggcc

27

<210> 466

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 466
 atcacccccga aggacgtcca ggagaag

27

<210> 467

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 467
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420

atcctcaccg	cgcaccgcga	cctctacca	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccgaagggc	acctcatcac	cccgaaggac	gtccaggaga	agtacggggg	gcccccgag	540
cgctgggtgg	acttccgcgc	cctcacgggg	gaccgctcgg	acaacatccc	cggggtggcg	600
gggatagggg	agaagaccgc	ccttcgactc	ctcgcagagt	gggggagcgt	ggaaaacctc	660
ctgaagaacc	tggaccgggt	aaagccggac	tcgctccggc	gcaagataga	ggcgcacctc	720
gaggacctcc	acctctcctt	agacctggcc	cgcattccga	ccgacctccc	cctggagggtg	780
gactttaagg	ccctgcgccg	caggaccccc	gacctggagg	gcctgagggc	ctttttggag	840
gagctggagt	tcggaagcct	cctccacgag	ttcggcctcc	tgggagggga	gaagccccgg	900
gaggaggccc	cctggcccc	gcccgaaggg	gccttcgtgg	gcttcctcct	ttcccgaag	960
gagcccatgt	gggcggagct	tctggccctg	gcggcggcct	cgggcggccg	cgtgcaccgg	1020
gcagcagacc	ccttggcggg	gctaaaggac	ctcaaggagg	tccggggcct	cctcgccaag	1080
gacctcgccg	tcttggcctc	gagggagggg	ctagacctcg	tgcccgggga	cgaccccatg	1140
ctcctcgcct	acctcctgga	cccttcgaac	accacccccg	aggggggtgg	gcggcgctac	1200
gggggggagt	ggacggagga	cgccgccac	cgggcctcc	tctcgagag	gctccatcg	1260
aacctcctta	agcgcctcga	gggggaggag	aagctccttt	ggctctacca	cgagggtgaa	1320
aagccccctc	cccgggtcct	ggcccatatg	gaggccaccg	gggtacggcg	ggacgtggcc	1380
taccttcagg	ccctttccct	ggagcttgcg	gaggagatcc	gccgcctcga	ggaggaggtc	1440
ttccgcttgg	cgggccaccc	cttcaacctc	aactcccggg	accagctgga	aaggggtgctc	1500
tttgacgagc	ttaggcttcc	cgccttgaag	aagacgaaga	agacaggcaa	gcgctccacc	1560
agcgcgcggg	tgttgagggc	cctacgggag	gcccacccca	tcgtggagaa	gatcctccag	1620
caccgggagc	tcaccaagct	caagaacacc	tacgtggacc	ccctcccaag	cctcgtccac	1680
ccgaggacgg	gccgcctcca	caccgccttc	aaccagacgg	ccacggccac	ggggaggcctt	1740
agtagctccg	accccaacct	gcagaacatc	cccgctccga	cccccttggg	ccagaggatc	1800
cgcggggcct	tcgtggccga	ggcgggttgg	gcgttggtgg	ccctggacta	tagccagata	1860
gagctccgcg	tcctcgccca	cctctccggg	gacgaaaacc	tgatcagggt	cttccaggag	1920
gggaaggaca	tcacacccca	gaccgcaagc	tggatgttcg	gcgtcccccc	ggaggccgtg	1980
gacccccctg	tgcgccgggc	ggccaagacg	gtgaacttcg	gcgtcctcta	cggcattgtcc	2040
gcccattagg	tctcccagga	gcttgccatc	ccctacgagg	aggcgggtgg	ctttatagag	2100
cgtacttcc	aaagcttccc	caagggtcgg	gcctggatag	aaaagaccct	ggaggagggg	2160
aggaagcggg	gctacgtgga	aaccctcttc	ggaagaaggc	gctacgtgcc	cgacctcaac	2220
gcccgggtga	agagcgtcag	ggaggccgcg	gagcgcattg	ccttcaacat	gcccgtccag	2280

ggcaccgccc cgcacctcat gaagctcgcc atggtgaagc tcttcccccg cctccgggag 2340
atggggggccc gcatgctcct ccaggtcgcc aacgagctcc tcctggaggc cccccaagcg 2400
cgggccgagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
gtgcccctgg aggtggagggt ggggatgggg gaggactggc tttccgcaa gggtcaccac 2520
caccaccacc ac 2532

<210> 468

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly
 165 170 175

Val Pro Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg
 180 185 190

Ser Asp Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Arg Leu Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu
 225 230 235 240

Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu
 260 265 270

Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu
 275 280 285

His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro
 290 295 300

Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys
 305 310 315 320

Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly
 325 330 335

Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys
 340 345 350

Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365

Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380

Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400

Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430
 Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460
 Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro

645					650					655					
Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn
			660					665					670		
Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu
		675					680					685			
Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln
	690					695					700				
Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly
705						710					715				720
Arg	Lys	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val
				725					730					735	
Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg
			740					745					750		
Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys
		755					760					765			
Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg
	770					775					780				
Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala
785						790					795				800
Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala
				805					810					815	
Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp
			820					825					830		
Trp	Leu	Ser	Ala	Lys	Gly	His	His	His	His	His	His	His	His	His	His
		835					840								

<210> 469

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 469
ctcgaggcgg gtaaacccca ggaggtc 27

<210> 470

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470
gggtttaccc gcctcgaggc gcccggc 27

<210> 471

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
ctcatcaagg agctgggtgga cctcctgggg ttaccgcc tcgaggtgcc gggctttgaa 360
gcggatgacg tcttggtac cctggccaag aaggcggaaa aggaaggcta cgaagtgcgc 420
atcctcaccg cggaccggga ctttaccag cttctttcgg agcgaatctc catccttcac 480
ccggaggggtt acctgatcac cccggagtgg ctttgggaga agtatgggct taagccttcc 540
cagtgggtgg actaccgggc cttggccggg gacccttcg acaacatccc cggcgtgaag 600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt 660
cttaagcacc tggaacaggc gaaacctgcc tccgtgcggg agaagatcct tagccacatg 720

gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcaggtg	780
gacttcgccc ggcgccggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcgga gacctctcca cgagttcggc ctgttgga aa gcccggtggc ggcggaggaa	900
gctccctggc cccccccga gggagccttc gtgggggtacg ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcggtgccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc ccgagggggg tggcgcgggc ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctcccggg tcttgccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcggtg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg	1680
acgggcgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggcccttg actatagcca gatagagctc	1860
cgcgtcctcg ccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaa	1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgccaa gacggtgaac ttcggcgctc tctacggcat gtccgccc	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccagggt gcgggccttg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacct caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tctccagggt cgccaacgag ctctcctcgg agggcccca agcgcggggc	2400
gaggagggtg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 472

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 472

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His
145 150 155 160

Pro Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro
180 185 190

Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala
 195 200 205

Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
 210 215 220

Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
 225 230 235 240

Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
 245 250 255

Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met

435		440		445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser				
450		455		460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg				
465		470		475
				480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg				
		485		490
				495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys				
		500		505
				510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu				
		515		520
				525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys				
		530		535
				540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg				
		545		550
				555
				560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly				
		565		570
				575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr				
		580		585
				590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp				
		595		600
				605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala				
		610		615
				620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys				
		625		630
				635
				640
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu				
		645		650
				655
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly				
		660		665
				670
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile				
		675		680
				685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 473

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

aagccactcc ggggtgatca ggtaacc

27

<210> 474

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

atcaccccgagg agtggctttg ggagaag

27

<210> 475

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctgggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcc accagaccta cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcacc cggagtggct ttgggagaag tacggcctca ggccggagca gtgggtggac	540
ttccgcgccc tcgtggggga cccctccgac aacctccccg ggggtcaaggg catcggggag	600
aagaccgccc tcaagctcct caaggagtgg ggaagcctgg aaaacctcct caagaacctg	660
gaccgggtaa agccagaaaa cgtccgggag aagatcaagg cccacctgga agacctcagg	720
ctctccttgg agctctcccg ggtgcgcacc gacctcccc tggaggtgga cctcgcccag	780
gggcgggagc ccgaccggga ggggcttagg gccttcctgg agaggctgga gttcggcagc	840
ctctccacg agttcggcct cctggaggcc cccgcccccc tggaggaggc cccctggccc	900
ccgccggaag gggccttcgt gggcttcgtc ctctcccgcc ccgagcccat gtgggcggag	960
cttaaagccc tggccgcctg caggggcggc cgcgtgcacc gggcagcaga ccccttggcg	1020

gggctaaagg	acctcaagga	ggtccggggc	ctcctcgcca	aggacctcgc	cgtcttgggc	1080
tcgagggagg	ggctagacct	cgtgcccggg	gacgacccca	tgctcctcgc	ctacctcctg	1140
gacccttcga	acaccacccc	cgaggggggtg	gcgcggcgct	acggggggga	gtggacggag	1200
gacgcgcgcc	accggggccct	cctctcggag	aggctccatc	ggaacctcct	taagcgctc	1260
gagggggagg	agaagctcct	ttggctctac	cacgagggtg	aaaagcccct	ctcccgggtc	1320
ctggcccata	tggaggccac	cggggtacgg	cgggacgtgg	cctaccttca	ggccctttcc	1380
ctggagcttg	cggaggagat	ccgccgcctc	gaggaggagg	tcttccgctt	ggcgggccac	1440
cccttcaacc	tcaactcccg	ggaccagctg	gaaaggggtg	tctttgacga	gcttaggctt	1500
cccgcttga	agaagacgaa	gaagacaggc	aagcgctcca	ccagcgccgc	ggtgctggag	1560
gccctacggg	aggcccaccc	catcgtggag	aagatcctcc	agcaccggga	gctcaccaag	1620
ctcaagaaca	cctacgtgga	ccccctcca	agcctcgctc	acccgaggac	gggccgcctc	1680
cacaccgct	tcaaccagac	ggccacggcc	acggggaggc	ttagtagctc	cgaccccaac	1740
ctgcagaaca	tccccgtccg	cacccccttg	ggccagagga	tccgccgggc	cttcgtggcc	1800
gaggcggtt	gggcgttgg	ggccctggac	tatagccaga	tagagctccg	cgctcctcgc	1860
cacctctccg	gggacgaaaa	cctgatcagg	gtcttccagg	aggggaagga	catccacacc	1920
cagaccgcaa	gctggatgtt	cggcgtcccc	ccggaggccg	tggaccccct	gatgcgccgg	1980
gcggccaaga	cggatgaactt	cggcgtcctc	tacggcatgt	ccgcccatag	gctctcccag	2040
gagcttgcca	tccccctacga	ggaggcggtg	gcctttatag	agcgctactt	ccaaagcttc	2100
cccaagggtg	gggcctggat	agaaaagacc	ctggaggagg	ggaggaagcg	gggctacgtg	2160
gaaaccctct	tcggaagaag	gcgctacgtg	ccgcacctca	acgcccgggt	gaagagcgtc	2220
agggaggccg	cggagcgcat	ggccttcaac	atgcccgtcc	agggcaccgc	cgccgacctc	2280
atgaagctcg	ccatggtgaa	gctcttcccc	cgcctccggg	agatgggggc	ccgcatgctc	2340
ctccaggctg	ccaacgagct	cctcctggag	gccccccaag	cgcggggcca	ggagggtggc	2400
gctttggcca	aggaggccat	ggagaaggcc	tatccccctc	ccgtgcccct	ggagggtggag	2460
gtggggatgg	gggaggactg	gctttccgcc	aagggtcacc	accaccacca	ccac	2514

<210> 476

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Glu
165 170 175

Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val Lys
210 215 220

Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp Leu Arg
225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp

				485					490					495		
Glu	Leu	Arg	Leu 500	Pro	Ala	Leu	Lys	Lys 505	Thr	Lys	Lys	Thr	Gly 510	Lys	Arg	
Ser	Thr	Ser 515	Ala	Ala	Val	Leu	Glu 520	Ala	Leu	Arg	Glu	Ala 525	His	Pro	Ile	
Val	Glu 530	Lys	Ile	Leu	Gln	His 535	Arg	Glu	Leu	Thr	Lys 540	Leu	Lys	Asn	Thr	
Tyr 545	Val	Asp	Pro	Leu	Pro 550	Ser	Leu	Val	His	Pro 555	Arg	Thr	Gly	Arg	Leu 560	
His	Thr	Arg	Phe	Asn 565	Gln	Thr	Ala	Thr	Ala 570	Thr	Gly	Arg	Leu	Ser 575	Ser	
Ser	Asp	Pro	Asn 580	Leu	Gln	Asn	Ile	Pro 585	Val	Arg	Thr	Pro	Leu 590	Gly	Gln	
Arg	Ile	Arg 595	Arg	Ala	Phe	Val	Ala 600	Glu	Ala	Gly	Trp	Ala 605	Leu	Val	Ala	
Leu	Asp 610	Tyr	Ser	Gln	Ile	Glu 615	Leu	Arg	Val	Leu	Ala 620	His	Leu	Ser	Gly	
Asp 625	Glu	Asn	Leu	Ile	Arg 630	Val	Phe	Gln	Glu	Gly 635	Lys	Asp	Ile	His	Thr 640	
Gln	Thr	Ala	Ser	Trp 645	Met	Phe	Gly	Val	Pro 650	Pro	Glu	Ala	Val	Asp 655	Pro	
Leu	Met	Arg	Arg 660	Ala	Ala	Lys	Thr	Val 665	Asn	Phe	Gly	Val	Leu 670	Tyr	Gly	
Met	Ser	Ala 675	His	Arg	Leu	Ser	Gln 680	Glu	Leu	Ala	Ile	Pro 685	Tyr	Glu	Glu	
Ala 690	Val	Ala	Phe	Ile	Glu	Arg 695	Tyr	Phe	Gln	Ser	Phe 700	Pro	Lys	Val	Arg	
Ala 705	Trp	Ile	Glu	Lys	Thr 710	Leu	Glu	Glu	Gly	Arg 715	Lys	Arg	Gly	Tyr	Val 720	
Glu	Thr	Leu	Phe	Gly 725	Arg	Arg	Arg	Tyr	Val 730	Pro	Asp	Leu	Asn 735	Ala	Arg	

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
770 775 780

Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
785 790 795 800

Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
820 825 830

His His His His His His
835

<210> 477

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 477

caccaccacc accaccacgt cgactagtgc tagcgtcgac tagctgcagg catgcaagct

60

tggc

64

<210> 478

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 478
gccaagcttg catgcctgca gctagtcgac gctagcacta gtcgacgtgg tggagggtgg 60
ggtg 64

<210> 479

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 479
caggaagcgg ccgcgtcgac atgaccatga ttacgccaag c 41

<210> 480

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 480
gggcccgcga gggtcgactc agggcgatgg ccactacgt ga 42

<210> 481

<211> 3135

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 481
atgaattccg aggcgatgct tccgtctttt gaacccaaag gccgggtcct cctgggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg	cogtcttcgt	ggtctttgac	gccaaaggccc	cctccttccg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgaggtccc	cggctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaag	aggaggggta	cgaggtgcgc	420
atcctcaccg	ccgaccgga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgtcctccac	480
cccaggggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggggtgcgc	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggaggga	gcccagaccg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagagggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccaccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggcccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggagggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040


```

aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagg gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcact caacgcccgg 2220
gtgaagagcg tcagggaggg cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctctctgg agggccccc aagcgggggc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccacgtcg acatgaccat gattacgcca agctatttag gtgacactat agaatactca 2580
agctatgcat caagcttggg accgagctcg gatccactag taacggccgc cagtgtgctg 2640
gaattctgca gatatccatc aactggcgg ccgctcgagc atgcatctag agggcccaat 2700
tcgccctata gtgagtcgta ttacaattca ctggccgctg ttttacaacg tcgtgactgg 2760
gaaaaccctg gcgttaccga acttaatcgc cttgcagcac atcccccttt cgccagctgg 2820
cgtaatagcg aagaggcccg caccgatcgc ctttcccaac agttgcgcag cctgaatggc 2880
gaatgggacg cgccctgtag cggcgcatta agcgcgggcg gtgtggtggt tacgcgcagc 2940
gtgaccgcta cacttgccag cgccctagcg cccgctcctt tcgctttctt cccttccttt 3000
ctcgccacgt tcgccggctt tcccgtcaa gctctaaatc gggggctccc tttagggttc 3060
cgatttagag ctttacggca cctcgaccgc aaaaaacttg atttgggtga tggttcacgt 3120
agtgggcat cgccc 3135

```

<210> 482

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

```

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1           5           10          15

```

```

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
          20          25          30

```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys

530		535		540
Leu 545	Lys	Asn	Thr	Tyr
		Val 550	Asp	Pro
			Leu	Pro
			Ser 555	Leu
			Val	His
			Pro	Arg 560
Thr	Gly	Arg	Leu	His
		Thr 565	Arg	Phe
			Asn	Gln 570
			Thr	Ala
			Thr	Ala
			Thr	Gly 575
Arg	Leu	Ser	Ser	Ser
		580	Asp	Pro
			Asn	Leu
			Gln 585	Asn
			Ile	Pro
			Val	Arg
			Thr	
Pro	Leu	Gly	Gln	Arg
		595	Ile	Arg
			Arg	Ala
			Phe	Val
			Ala	Glu
			Ala	Gly
			Trp	
Ala	Leu	Val	Ala	Leu
		610	Asp	Tyr
			Ser	Gln
			Ile	Glu
			Leu	Arg
			Val	Leu
			Ala	
His	Leu	Ser	Gly	Asp
			Glu	Asn
			Leu	Ile
			Arg	Val
			Phe	Gln
			Glu	Gly
			Lys	
				640
Asp	Ile	His	Thr	Gln
			Thr	Ala
			Ser	Trp
			Met	Phe
			Gly	Val
			Pro	Pro
			Glu	
				655
Ala	Val	Asp	Pro	Leu
			Met	Arg
			Arg	Ala
			Ala	Lys
			Thr	Val
			Asn	Phe
			Gly	
				670
Val	Leu	Tyr	Gly	Met
			Ser	Ala
			His	Arg
			Leu	Ser
			Gln	Glu
			Leu	Ala
			Ile	
				685
Pro	Tyr	Glu	Glu	Ala
			Val	Ala
			Phe	Ile
			Glu	Arg
			Tyr	Phe
			Gln	Ser
			Phe	
				690
Pro	Lys	Val	Arg	Ala
			Trp	Ile
			Glu	Lys
			Thr	Leu
			Glu	Glu
			Gly	Arg
			Lys	
				720
Arg	Gly	Tyr	Val	Glu
			Thr	Leu
			Phe	Gly
			Arg	Arg
			Arg	Tyr
			Val	Pro
			Asp	
				735
Leu	Asn	Ala	Arg	Val
			Lys	Ser
			Val	Arg
			Glu	Ala
			Ala	Glu
			Arg	Met
			Ala	
				740
Phe	Asn	Met	Pro	Val
			Gln	Gly
			Thr	Ala
			Ala	Asp
			Leu	Met
			Lys	Leu
			Ala	
				755
Met	Val	Lys	Leu	Phe
			Pro	Arg
			Leu	Arg
			Glu	Met
			Gly	Ala
			Arg	Met
			Leu	
				770
				780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly His His His His His His Val Asp Met Thr Met Ile
 835 840 845

Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser Ser Tyr Ala Ser
 850 855 860

Ser Leu Val Pro Ser Ser Asp Pro Leu Val Thr Ala Ala Ser Val Leu
 865 870 875 880

Glu Phe Cys Arg Tyr Pro Ser His Trp Arg Pro Leu Glu His Ala Ser
 885 890 895

Arg Gly Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala
 900 905 910

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
 915 920 925

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
 930 935 940

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
 945 950 955 960

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
 965 970 975

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala
 980 985 990

Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro
 995 1000 1005

Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Phe Arg Phe Arg
 1010 1015 1020

Ala Leu Arg His Leu Asp Arg Lys Lys Leu Asp Leu Gly Asp Gly
 1025 1030 1035

Ser Arg Ser Gly Pro Ser Pro
1040 1045

<210> 483

<211> 36,

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

cgggacctcg aggcgcgtga accccaggag gtccac

36

<210> 484

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag	120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720

aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgccctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgccgg	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cgccggggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgt	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcggt	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggcccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaaag	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccgacc	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgcccac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccccatg	2340
ctcctccagg	tcgccaacga	gctcctcctg	gaggcccccc	aagcgcgggc	cgaggagggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460
gagggtgggga	tgggggagga	ctggcctttcc	gccaagggtc	accaccacca	ccaccac	2517

<210> 485

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val

690	695	700
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr 705 710 715 720		
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala 725 730 735		
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750		
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765		
Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val 770 775 780		
Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val 785 790 795 800		
Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val 805 810 815		
Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys 820 825 830		
Gly His His His His His His 835		

<210> 486

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

gtggaccttc tgggctttac ccgcctcgag gccccg

36

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

cggggcctcg aggcgggtaa agcccagaag gtccac

36

<210> 488

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160

Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175

Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190

Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205

Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255

Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly

385		390		395		400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu	405			410		415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp	420			425		430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met	435			440		445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser	450			455		460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg	465			470		475
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg	485			490		495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys	500			505		510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu	515			520		525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys	530			535		540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg	545			550		555
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly	565			570		575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr	580			585		590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp	595			600		605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala	610			615		620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys	625			630		635
						640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly His His His His His His
 835 840

<210> 489

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

tttaccgcgcc tcgagggtgcc gggc

24

<210> 490

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

cggcacctcg aggcgggtaa agcccaaaag gtccac

36

<210> 491

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 491

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
 130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
 145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445

Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln

580					585					590					
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala
		595					600					605			
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly
	610					615					620				
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr
625						630					635				640
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro
				645					650					655	
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly
			660					665					670		
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu
		675					680					685			
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
	690					695					700				
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val
705						710					715				720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala
	770					775					780				
Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala
785						790					795				800
Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly
			820					825					830		

His His His His His His
835

<210> 492

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 492

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 493

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 493

ggaaggaggg ggcctcggcg tcaaagacca cgat

34

<210> 494

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60
 Val Phe Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu

275					280					285					
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
290						295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu
	370					375					380				
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly
385					390					395					400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu
				405					410					415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp
			420					425					430		
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met
		435					440					445			
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
	450					455					460				
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
465					470					475					480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
				485					490					495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys
			500					505					510		
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
		515					520					525			

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser, Ala Lys Gly His His His His His His
 835 840

<210> 495

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 495

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtcct tgacgccgag gccccctcct tccgccacga ggccctacggg	240
gggtacaagg cgggcccgggc cccacgcccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacccctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac	600
ggggagaaga cggcgaggaa gcttctggag gaggggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caagggtgag accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggcct agggcctttc tggagagggt tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900

ccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcttacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccg	1320
gtcctggccc	atatggaggc	caccggggta	cgcggggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcggt	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccct	ccaagcctcg	tccacccgag	gacggggccg	1680
ctccacaccc	gcttcaacca	gacggccaag	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccgacc	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcacg	2340
ctcctccagg	tcgccaacga	gctcctcctg	gaggcccccc	aagcgcgggc	cgaggagggtg	2400
gcggctttgg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460
gaggtggggg	tgggggagga	ctggctttcc	gccaagggtc	accaccacca	ccaccac	2517

<210> 496

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190 \

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly

465		470		475		480									
His	Pro	Phe	Asn	Leu	Asn	Pro	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn
	530					535					540				
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His
625					630					635					640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 497

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac	60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag	120
ccggtgcaga tgggtctacgg cttcgcccg agcctcctca aggccttgaa ggaggacgga	180
caggcggtgg tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacgag	240
gcctacaagg cgggcccggc cccacccccg gaggacttcc cccgccagct cgccttggtc	300
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac	360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcacctc	420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac	480

gggaccctgg	tcaccccaaa	ggacgtccag	gagaagtacg	gggtgcccc	ggagcgctgg	540
gtggacttcc	gcgccctcac	gggggaccgc	tcggacaaca	tccccggggt	ggcggggata	600
ggggagaaga	ccgcccttcg	actcctcgca	gagtggggga	gcgtggaaaa	cctcctgaag	660
aacctggacc	gggtaaaagcc	ggactcgctc	cggcgcaaga	tagaggcgca	cctcgaggac	720
ctccacctct	ccttagacct	ggcccgcatc	cgcaccgacc	tccccctgga	ggtggacttt	780
aaggccctgc	gccgcaggac	ccccgacctg	gagggcctga	gggccttttt	ggaggagctg	840
gagttcggaa	gcctcctcca	cgagttcggc	ctcctggggag	gggagaagcc	ccgggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcc	tcctttcccg	caaggagccc	960
atgtgggcgg	agcttctggc	cctggcggcg	gcctcggggc	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgccct	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggccac	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccaccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaa	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaagg	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340

gccccgatgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaaggggtca ccaccaccac 2520
caccac 2526

<210> 498

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 498

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp

145					150					155					160
Gly	Thr	Leu	Val	Thr	Pro	Lys	Asp	Val	Gln	Glu	Lys	Tyr	Gly	Val	Pro
				165					170					175	
Pro	Glu	Arg	Trp	Val	Asp	Phe	Arg	Ala	Leu	Thr	Gly	Asp	Arg	Ser	Asp
			180					185					190		
Asn	Ile	Pro	Gly	Val	Ala	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Arg	Leu
		195					200					205			
Leu	Ala	Glu	Trp	Gly	Ser	Val	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Asp	Ser	Leu	Arg	Arg	Lys	Ile	Glu	Ala	His	Leu	Glu	Asp
225					230					235					240
Leu	His	Leu	Ser	Leu	Asp	Leu	Ala	Arg	Ile	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	
Glu	Val	Asp	Phe	Lys	Ala	Leu	Arg	Arg	Arg	Thr	Pro	Asp	Leu	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Gly	Gly	Glu	Lys	Pro	Arg	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu	Ser	Arg	Lys	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Ser	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu
	370					375					380				
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly
385					390					395					400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 499

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 499
 atgaattccc tgccctcttt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60
 ctggcctacc gtaccttttt tgccctgaag ggccctacca ccagccgcgg ggagccggtc 120
 caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180
 gtgatcgtgg tctttgacgc cgaggccccc tcttccgcc accagacctt cgaggcctac 240
 aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag 300
 atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc 360
 ctggctaccc tggccaagaa ggcggaagaa gaaggctacg aagtgcgcat cctcaccgcg 420
 gaccgggacc tttaccagct tctttcggag cgaatctcca tcttccccc ggagggttac 480
 ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540
 taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag 600
 aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg 660
 gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag 720
 ctatccctgg agctatcccc ggtgcacacg gacttgctcc ttcagggtgga cttcgcccg 780
 cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcggaagc 840
 ctctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg 900
 ccccccagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag 960
 cttaacgcct tggccgccgc ctggggcgcc cgcgtgcacc gggcagcaga ccccttggcg 1020
 gggctaaagg acctcaagga ggtccggggc ctctcgcca aggacctgc cgtcttggcc 1080
 tcgagggagg ggctagacct cgtgcccggg gacgaccca tgctcctcgc ctacctcctg 1140
 gacccttoga acaccacccc cgagggggtg gcgcggcgct acggggggga gtggacggag 1200
 gacgcccgc accgggccct cctctcggag aggtccatc ggaacctcct taagcgcctc 1260
 gagggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccgggtc 1320
 ctggcccata tggaggccac cggggtacgg cgggacgtgg cctaccttca ggcctttcc 1380
 ctggagcttg cggaggagat ccgcccctc gaggaggagg tcttccgctt ggcgggccac 1440
 cccttcaacc tcaactcccc ggaccagctg gaaaggggtg tctttgacga gcttaggctt 1500
 cccgccttga agaagacgaa gaagacaggc aagcgtcca ccagcgccgc ggtgctggag 1560
 gccctacggg agggccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag 1620
 ctcaagaaca cctacgtgga cccctccca agcctcgtcc acccgaggac gggccgcctc 1680
 cacaccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac 1740
 ctgcagaaca tccccgtccg ccccccttg ggccagagga tccgcccggc cttcgtggcc 1800
 gaggcggggt gggcggttgt ggccctggac tatagccaga tagagctccg cgtcctcgcc 1860

cacctctccg gggacgaaaa cctgatcagg gtcttccagg aggggaagga catccacacc 1920
cagaccgcaa gctggatggt cggcgtcccc ccggaggccg tggaccccct gatgcgccg 1980
gcgccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag gctctcccag 2040
gagcttgcca tcccctacga ggaggcgggt gcctttatag agcgctactt ccaaagcttc 2100
ccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg 2160
gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220
agggaggccg cggagcgcgt ggccttcaac atgcccgctc agggcaccgc cgccgacctc 2280
atgaagctcg ccatggtgaa gctcttcccc cgcctccggg agatgggggc ccgcatgctc 2340
ctccaggctg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg 2400
gctttggcca aggaggccat ggagaaggcc tatccccctg ccgtgcccct ggaggtggag 2460
gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac 2514

<210> 500

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 500

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
 165 170 175
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
 210 215 220
 Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240
 Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445

Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala

595		600		605
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly	610	615	620	
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr	625	630	635	640
Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro	645	650	655	
Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly	660	665	670	
Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu	675	680	685	
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg	690	695	700	
Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val	705	710	715	720
Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg	725	730	735	
Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro	740	745	750	
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu	755	760	765	
Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala	770	775	780	
Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala	785	790	795	800
Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro	805	810	815	
Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly	820	825	830	
His His His His His His	835			

<210> 501

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 501

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccc gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ctttctggaa agccccaaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcgggggctaa aggacctcaa ggaggtccgg ggctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgcc ggggacgacc ccatgctcct cgcctacctc	1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccg cccaccgggc ctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cttttggctc taccacgagg tggaaaagcc cctctcccg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc	1440

caccctttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacgggccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccg ggccttcgtg 1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
accagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccgaac tcaacgcccg ggtgaagagc 2220
gtcaggaggc ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
ctcatgaagc tcgccatggg gaagctcttc ccccgccctc gggagatggg ggcccgcacg 2340
ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggagggtg 2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
gagggtgggga tgggggagga ctggccttcc gccaaagggtc accaccacca ccaccac 2517

<210> 502

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe

35					40					45					
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
50					55						60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val

785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 503

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 503

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 504

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 504

ggaaggaggg ggcctcggcg tcaaagacca cgat

34

<210> 505

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 505

atgaattcgg	aggcgatgct	gccccctcttt	gagcccaagg	gccgggtcct	cctggtggac	60
ggccaccacc	tggcctaccg	caccttccac	gccctgaagg	gcctcaccac	cagccggggg	120
gagccggtgc	aggcggtcta	cggttcgcc	aagagcctcc	tcaaggccct	caaggaggac	180
ggggacgcgg	tgatcgtggt	ctttgacgcc	gaggccccct	ccttccgcca	cgaggcctac	240
ggggggtaca	aggcgggccc	ggccccccacg	ccggaggact	ttccccggca	actcgccctc	300
atcaaggagc	tggtggacct	cctgggggttc	acgcgcctcg	aggtcccggg	ctacgaggcg	360
gacgacgtcc	tggccagcct	ggccaagaag	gcggaaaagg	agggctacga	ggtccgcatac	420
ctcaccgccc	acaaagacct	ttaccagctc	ctttccgacc	gcatccacgt	cctccacccc	480
gaggggtacc	tcatcacccc	ggcctggctt	tgggaaaagt	acggcctgag	gcccgaccag	540
tgggcccact	accgggcccct	gaccggggac	gagtccgaca	accttcccgg	ggtcaagggc	600
atcggggaga	agacggcgag	gaagcttctg	gaggagtggg	ggagcctgga	agccctcctc	660
aagaacctgg	accggtgaa	gcccgccatc	cgggagaaga	tcctggccca	catggacgat	720
ctgaagctct	cctgggacct	ggccaagggtg	cgcaccgacc	tgccccctgga	ggtggacttc	780
gccaaaaggc	gggagcccga	ccgggagagg	cttagggcct	ttctggagag	gcttgagttt	840
ggcagcctcc	tccacgagtt	cggccttctg	gaaagcccca	aggccctgga	ggaggccccc	900
tggccccccg	cggaaggggc	cttcgtgggc	tttgtgcttt	cccgcaagga	gcccattgtg	960
gccgatcttc	tggccctggc	cgccgccagg	ggcggccgcg	tgcaccgggc	agcagacccc	1020
ttggcggggc	taaaggacct	caaggaggtc	cggggcctcc	tcgccaagga	cctcgccgtc	1080
ttggcctoga	gggaggggct	agacctcgtg	cccggggacg	accccatgct	cctcgccctac	1140
ctcctggacc	cttcgaacac	cacccccgag	ggggtggcgc	ggcgctacgg	gggggagtg	1200
acggaggacg	ccgcccaccg	ggccctcctc	tcggagaggc	tccatcgga	cctccttaag	1260
cgcctcgagg	gggaggagaa	gctccttttg	ctctaccacg	aggtggaaaa	gcccctctcc	1320
cgggtcctgg	cccatatgga	ggccaccggg	gtacggcggg	acgtggccta	ccttcaggcc	1380
ctttccctgg	agcttgcgga	ggagatccgc	cgcctcgagg	aggaggtctt	ccgcttggcg	1440
ggccacccct	tcaacctcaa	ctcccgggac	cagctggaaa	gggtgctctt	tgacgagctt	1500
aggcttccc	ccttgaagaa	gacgaagaag	acaggcaagc	gctccaccag	cgccgcggtg	1560
ctggaggccc	tacgggaggc	ccaccccatc	gtggagaaga	tcctccagca	ccgggagctc	1620
accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttggggc	agaggatccg	ccgggccttc	1800

gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860
 ctcgcccacc tctccgggga cgaaaacctg atcaggggtct tccaggaggg gaaggacatc 1920
 cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg 1980
 cgccggggcg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc 2040
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160
 tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccgc 2340
 atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 506

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 506

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
 50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
 65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg

				85				90						95		
Gln	Leu	Ala	Leu 100	Ile	Lys	Glu	Leu	Val 105	Asp	Leu	Leu	Gly	Phe 110	Thr	Arg	
Leu	Glu	Val 115	Pro	Gly	Tyr	Glu	Ala 120	Asp	Asp	Val	Leu	Ala 125	Ser	Leu	Ala	
Lys	Lys 130	Ala	Glu	Lys	Glu	Gly 135	Tyr	Glu	Val	Arg	Ile 140	Leu	Thr	Ala	Asp	
Lys 145	Asp	Leu	Tyr	Gln	Leu 150	Leu	Ser	Asp	Arg	Ile 155	His	Val	Leu	His	Pro 160	
Glu	Gly	Tyr	Leu	Ile 165	Thr	Pro	Ala	Trp	Leu 170	Trp	Glu	Lys	Tyr	Gly 175	Leu	
Arg	Pro	Asp	Gln 180	Trp	Ala	Asp	Tyr	Arg 185	Ala	Leu	Thr	Gly	Asp 190	Glu	Ser	
Asp	Asn	Leu 195	Pro	Gly	Val	Lys	Gly 200	Ile	Gly	Glu	Lys	Thr 205	Ala	Arg	Lys	
Leu	Leu 210	Glu	Glu	Trp	Gly	Ser 215	Leu	Glu	Ala	Leu	Leu 220	Lys	Asn	Leu	Asp	
Arg 225	Leu	Lys	Pro	Ala	Ile 230	Arg	Glu	Lys	Ile	Leu 235	Ala	His	Met	Asp	Asp 240	
Leu	Lys	Leu	Ser	Trp 245	Asp	Leu	Ala	Lys	Val 250	Arg	Thr	Asp	Leu	Pro 255	Leu	
Glu	Val	Asp	Phe 260	Ala	Lys	Arg	Arg	Glu 265	Pro	Asp	Arg	Glu	Arg 270	Leu	Arg	
Ala	Phe	Leu 275	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly	
Leu	Leu 290	Glu	Ser	Pro	Lys	Ala 295	Leu	Glu	Glu	Ala	Pro 300	Trp	Pro	Pro	Pro	
Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Lys	Glu	Pro	Met	Trp 320	
Ala	Asp	Leu	Leu	Ala 325	Leu	Ala	Ala	Ala	Arg 330	Gly	Gly	Arg	Val	His 335	Arg	

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly His His His His His His

835

840

<210> 507

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 507

cagaccatga attcggaggc gatgctgccc ctcttt

36

<210> 508

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 508

aaagaggggc agcatcgcct ccgaattcat ggtctg

36

<210> 509

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 509

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc

60

caccacctgg cctaccgcac cttctttgcc ctgaagggcc tcaccaccag ccgggggggag

120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg

240

gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgcctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caagggtcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggcct	agggcctttc	tggagaggct	tgagtttgcc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
ccccgcggg	aaggggcctt	cgtgggcctt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcgggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttccgcctt	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcggt	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccctc	ccaagcctcg	tccacccgag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttggggcaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacgggtgaa	cttcggcgtc	ctctacggca	tgtccgcccc	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100

ttccccaagg tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccc ggtgaagagc 2220
 gtcagggagg ccgcggagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcagc 2340
 ctctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His

625		630		635		640									
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val
785					790					795					800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val
				805					810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		
Gly	His	His	His	His	His	His									
		835													

<210> 511

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 511

gcctaccgca ccttctttgc cctgaagggc ctc

33

<210> 512

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 512

gaggcccttc agggcaaaga aggtgcggta ggc

33

<210> 513

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 513

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc

60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag

120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcag agaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg

240

gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cggcctcatc

300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac

360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc

420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag

480

gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg

540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac

600

ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcctt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggacctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccct	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttggggccaga	ggatccgccg	ggccttcgtg	1800
gccgagggcg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgac	agggtcttcc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccagacc	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatgg	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcatg	2340
ctcctccagg	tcgccaacga	gctcctcctg	gaggcccccc	aagcgcgggc	cgaggagggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460

gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu

675		680		685											
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
690						695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val
785					790					795					800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val
				805					810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		
Gly	His	His	His	His	His	His	His								
		835													

<210> 515

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 515

ctcctcaagg ccctcagaga ggacggggac gcg

33

<210> 516

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 516

cgcggtccccg tcctctctga gggccttgag gag

33

<210> 517

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 517

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcgggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccacctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttgcc	840
agcctcctcc acgagttcgg cttcttgga agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960

gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcttacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttcccgcc	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttggggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaaag	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaacc	tcttcggaag	aaggcgctac	gtgcccgacc	tcaacgccc	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgccc	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcgatg	2340
ctcctccagg	tcgccaacga	gctcctcctg	gaggcccccc	aagcgcgggc	cgaggagggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460
gaggtgggga	tgggggagga	ctggctttcc	gccaaagggtc	accaccacca	ccaccac	2517

<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala

[illegible]

33

<220>
<223> Synthetic

<400> 520
cgctttcttg gccaggggtg ccaggacgtc gtc

33

<210> 521

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 521
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg ctccgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600
ggggagaaga cggcgctcaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg cttcttgaa agccccaagg ccctggagga ggccccctgg 900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg. 1020
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320

gtccctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
 tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
 cttcccgct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560
 gagggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcac 1620
 aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
 aacctgcaga acatccccgt ccgcaccccc ttggggccaga ggatccgccg ggccttcgtg 1800
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
 gcccacctct ccggggacga aaacctgatc agggctcttc aggggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatcccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttcccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220
 gtcaggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgcgcggac 2280
 ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcag 2340
 ctctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 522

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys

20					25					30					
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
	35						40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
340 345 350
Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
355 360 365
Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400
Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
405 410 415
Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
420 425 430
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
435 440 445
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
450 455 460
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465 470 475 480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495
Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
500 505 510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val

770		775		780
Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val				
785		790	795	800
Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val				
	805		810	815
Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys				
	820		825	830
Gly His His His His His His				
	835			

<210> 523
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 523
 ggggagaaga cggcgctcaa gcttctggag gag

33

<210> 524
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 524
 ctctccaga agcttgagcg ccgtcttctc ccc

33

<210> 525
 <211> 2517
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 525

atgaattcgg	ggatgctgcc	cctctttgag	cccaagggcc	gggtcctcct	ggtggacggc	60
caccacctgg	cctaccgcac	cttcacgcc	ctgaagggcc	tcaccaccag	ccggggggag	120
ccggtgcagg	cggtctacgg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtggtctt	tgacgccgag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgcctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcctcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggt	caagggcctc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccat	ggacgatctg	720
aagctctcct	gggacctggc	caagggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggaggggctt	aaggcctttc	tggagagggt	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcgggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttcccgctt	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcggt	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccct	ccaagcctcg	tccacccgag	gacggggccg	1680

ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttggggccaga ggatccgccg ggccttcgtg 1800
gccgaggcgg gttgggcggtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
gcccacctct ccggggacga aaacctgac agggtcttcc aggaggggaa ggacatccac 1920
accagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcag 2340
ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 526

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 526

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly

65		70		75		80									
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
	195						200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
	275						280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys

	820	825	830
Gly His His His His His His			
835			
<210>	527		
<211>	39		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	527		
gagccccgacc gggaggggct taaggccttt ctggagagg			39
<210>	528		
<211>	39		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	528		
cctctccaga aaggccttaa gcccctcccg gtcgggctc			39
<210>	529		
<211>	2517		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Synthetic		
<400>	529		
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc			60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag			120

ccggtgcagg	cggtctacgg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtgggtctt	tgacgccgag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgccctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccag	480
gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcac	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caagggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggga	ggggagaagc	cccgggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttcccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccct	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggcccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gccccacctc	ccggggacga	aaacctgata	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980

cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggtctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgcacc tcaacgcccg ggtgaagagc 2220
 gtcaggaggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcacg 2340
 ctctccagg tcgccaacga gtcctcctg gagggcccc aagcgcgggc cgaggaggtg 2400
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 530

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser

610		615		620	
Gly 625	Asp	Glu	Asn	Leu	Ile 630
	Arg	Val	Phe	Gln	Glu 635
	Gly	Lys	Asp	Ile	His 640
Thr	Gln	Thr	Ala	Ser 645	Trp
	Met	Phe	Gly	Val 650	Pro
	Pro	Pro	Glu	Ala	Val 655
Pro	Leu	Met	Arg	Arg	Ala 660
	Ala	Lys	Thr	Val 665	Asn
	Phe	Gly	Val	Leu	Tyr 670
Gly	Met	Ser 675	Ala	His	Arg
	Leu	Ser 680	Gln	Glu	Leu
	Ala	Ile 685	Pro	Tyr	Glu
Glu	Ala	Val	Ala	Phe	Ile
690		Glu	Arg	Tyr	Phe
	Gln	Ser	Phe	Pro	Lys
	Val				
Arg	Ala	Trp	Ile	Glu	Lys
705		Thr	Leu	Glu	Glu
	Gly	Arg	Lys	Arg	Gly
	Tyr				
	Val	Pro	Asp	Leu	Asn
	Ala				
Val	Glu	Thr	Leu	Phe 725	Gly
	Arg	Arg	Arg	Tyr 730	Val
	Pro	Asp	Leu	Asn	Ala 735
Arg	Val	Lys	Ser 740	Val	Arg
	Glu	Ala	Ala 745	Glu	Arg
	Met	Ala	Phe	Asn	Met 750
Pro	Val	Gln	Gly	Thr	Ala
755		Ala	Asp	Leu	Met
	Lys	Leu	Ala	Met	Val
	Lys				
Leu	Phe	Pro	Arg	Leu	Arg
770		Glu	Met	Gly	Ala
	Arg	Met	Gly	Ala	Arg
	Leu	Leu	Gln	Val	
Ala	Asn	Glu	Leu	Leu	Leu
785		Glu	Ala	Pro	Gln
	Ala	Arg	Ala	Glu	Glu
	Val				
Ala	Ala	Leu	Ala	Lys	Glu
	Ala	Met	Glu	Lys	Ala
	Tyr	Pro	Leu	Ala	Val
Pro	Leu	Glu	Val	Glu	Val
820		Gly	Met	Gly	Glu
	Asp	Trp	Leu	Ser	Ala
	Lys				
Gly	His	His	His	His	His
835					
<210>	531				
<211>	54				

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531

cacgagttcg gccttctggg aggggagaag ccccgaggagg agggcccttg gccc 54

<210> 532

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532

gggccagggg gcctcctccc ggggcttctc ccctcccaga aggccgaact cgtg 54

<210> 533

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 533

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccgggggt	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcmc	accgacctgc	ccctggagggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcctt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	ctgcaggggc	ggccgcgtgc	accgggcagc	agaccccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgccgc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcmc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttcccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcmc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcggt	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccctc	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggcccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gccccacctt	ccggggacga	aaacctgata	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcccc	taggctctcc	2040
caggagcttg	ccatccccct	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccgaac	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccc	tccagggcac	cgccgcccga	2280
ctcatgaagc	tcgccatggg	gaagctcttc	ccccgcctcc	gggagatggg	ggccccgatg	2340

ctcctccagg tcgccaacga gtcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400
gcggcctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr

660						665						670					
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu		
		675					680					685					
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val		
	690					695					700						
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr		
705					710					715					720		
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala		
				725					730					735			
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met		
			740					745					750				
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys		
		755					760					765					
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val		
	770					775					780						
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val		
785					790					795					800		
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val		
				805					810					815			
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys		
			820					825					830				
Gly	His	His	His	His	His	His											
		835															

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535

ctggccctgg ccgcctgcag gggcggccgc gtg 33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536

cacgcggccg cccctgcagg cggccagggc cag 33

<210> 537

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 537

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggccgggc cccacgccc gaggactttc ccgggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600

ggggagaaga cggcgaggaa gcttctgaag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc	1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtgagcg	1200
gaggacgcg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcggggacg tggcctacct tcaggccctt	1380
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc	1440
caccccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcggt gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccaccgag gacgggcccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttggggccaga ggatccgccg ggccttcgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgac aggggtcttcc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac	2280
ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcgtg	2340
ctcctccagg tcgccaacga gtcctcctg gagggccccc aagcgcgggc cgaggaggtg	2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
gagggtgggga tgggggagga ctggccttcc gccaaagggtc accaccacca ccaccac	2517

<210> 538

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu

450		455		460											
Ala 465	Glu	Glu	Ile	Arg	Arg 470	Leu	Glu	Glu	Glu	Val 475	Phe	Arg	Leu	Ala	Gly 480
His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp	Gln 490	Leu	Glu	Arg	Val	Leu	Phe 495
Asp	Glu	Leu	Arg 500	Leu	Pro	Ala	Leu	Lys 505	Lys	Thr	Lys	Lys	Thr 510	Gly	Lys
Arg	Ser	Thr 515	Ser	Ala	Ala	Val	Leu 520	Glu	Ala	Leu	Arg	Glu 525	Ala	His	Pro
Ile	Val 530	Glu	Lys	Ile	Leu	Gln 535	His	Arg	Glu	Leu	Thr 540	Lys	Leu	Lys	Asn
Thr 545	Tyr	Val	Asp	Pro	Leu 550	Pro	Ser	Leu	Val	His 555	Pro	Arg	Thr	Gly	Arg 560
Leu	His	Thr	Arg	Phe 565	Asn	Gln	Thr	Ala	Thr 570	Ala	Thr	Gly	Arg	Leu	Ser 575
Ser	Ser	Asp	Pro 580	Asn	Leu	Gln	Asn	Ile 585	Pro	Val	Arg	Thr	Pro 590	Leu	Gly
Gln	Arg	Ile 595	Arg	Arg	Ala	Phe	Val 600	Ala	Glu	Ala	Gly	Trp 605	Ala	Leu	Val
Ala 610	Leu	Asp	Tyr	Ser	Gln	Ile 615	Glu	Leu	Arg	Val	Leu 620	Ala	His	Leu	Ser
Gly 625	Asp	Glu	Asn	Leu	Ile 630	Arg	Val	Phe	Gln	Glu 635	Gly	Lys	Asp	Ile	His 640
Thr	Gln	Thr	Ala	Ser 645	Trp	Met	Phe	Gly	Val 650	Pro	Pro	Glu	Ala	Val 655	Asp
Pro	Leu	Met	Arg 660	Arg	Ala	Ala	Lys	Thr 665	Val	Asn	Phe	Gly	Val 670	Leu	Tyr
Gly	Met	Ser 675	Ala	His	Arg	Leu	Ser 680	Gln	Glu	Leu	Ala	Ile 685	Pro	Tyr	Glu
Glu 690	Ala	Val	Ala	Phe	Ile	Glu 695	Arg	Tyr	Phe	Gln	Ser 700	Phe	Pro	Lys	Val

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 539

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 539

ggggagaaga cggcgaggaa gcttctgaag gagtggggga gc

42

<210> 540

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 540

gctccccac tccttcagaa gcttcctcgc cgtcttctcc cc

42

<210> 541

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 541

atgaattcgg aggcgatgct gcccctcttt gagcccaagg gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttt gccctgaagg gcctcaccac cagccggggg	120
gagccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct cagagaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc gagggccccct ccttccgcca cgaggcctac	240
ggggggtaca aggcggggccg ggccccccacg ccggaggact ttccccggca actcgccctc	300
atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcac	420
ctcaccgccc acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggccctggctt tgggaaaagt acggcctgag gcccgaccag	540
tgggccgact accgggcccct gaccggggac gaggccgaca accttcccgg ggtcaagggc	600
atcggggaga agacggcgct caagcttctg gaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaagggtg cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg ggagggggaga agccccggga ggaggcccc	900
tggccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140

ctcctggacc	cttcgaacac	cacccccgag	ggggtggcgc	ggcgctacgg	gggggagtgg	1200
acggaggacg	ccgcccaccg	ggccctcctc	tcggagaggc	tccatcggaa	cctccttaag	1260
cgcctcgagg	gggaggagaa	gctcctttgg	ctctaccacg	aggtggaaaa	gcccctctcc	1320
cgggtcctgg	cccatatgga	ggccaccggg	gtacggcggg	acgtggccta	ccttcaggcc	1380
ctttccctgg	agcttgcgga	ggagatccgc	cgcctcgagg	aggaggtctt	ccgcttggcg	1440
ggccaccctt	tcaacctcaa	ctcccgggac	cagctggaaa	gggtgctctt	tgacgagctt	1500
aggcttcccc	ccttgaagaa	gacgaagaag	acaggcaagc	gctccaccag	cgccgcgggtg	1560
ctggaggccc	tacgggaggc	ccaccccatc	gtggagaaga	tcctccagca	ccgggagctc	1620
accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgtttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttggggc	agaggatccg	ccgggccttc	1800
gtggccgagg	cgggttgggc	gttgggtggc	ctggactata	gccagataga	gctccgcgtc	1860
ctcgcccacc	tctccgggga	cgaaaacctg	atcaggggtct	tccaggaggg	gaaggacatc	1920
cacaccaga	ccgcaagctg	gatgttcggc	gtccccccgg	aggccgtgga	ccccctgatg	1980
cgcggggcgg	ccaagacggt	gaacttcggc	gtcctctacg	gcatgtccgc	ccataggctc	2040
tcccaggagc	ttgccatccc	ctacgaggag	gcggtggcct	ttatagagcg	ctacttccaa	2100
agcttcccc	aggtgcgggc	ctggatagaa	aagaccctgg	aggagggggag	gaagcggggc	2160
tacgtggaaa	ccctcttcgg	aagaaggcgc	tacgtgcccc	acctcaacgc	ccgggtgaag	2220
agcgtcaggg	aggccgcgga	gcgcatggcc	ttcaacatgc	ccgtccaggg	caccgccgcc	2280
gacctcatga	agctcgccat	ggtgaagctc	ttcccccgcc	tccgggagat	ggggggccgc	2340
atgctcctcc	aggtcgccaa	cgagctcctc	ctggaggccc	cccaagcgcg	ggccgaggag	2400
gtggcggtt	tggccaagga	ggccatggag	aaggcctatc	ccctcgccgt	gcccctggag	2460
gtggaggtgg	ggatggggga	ggactggctt	tccgccaagg	gtcaccacca	ccaccaccac	2520

<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
50 55 60
Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80
Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
115 120 125
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
195 200 205
Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
210 215 220
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
225 230 235 240
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly

500					505					510					
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His
		515					520					525			
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys
	530					535					540				
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly
545					550					555					560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
				565					570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu
		595					600					605			
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830

Lys Gly His His His His His His
835 840

<210> 543

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 543

atgaattcgg aggcgatgct gccctcttt gagcccaagg gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttt gccctgaagg gcctcaccac cagccggggg	120
gagccgggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc gagggccct ccttccgcc cgaggcctac	240
gggggggtaca aggcggggccg ggcccccacg ccggaggact ttccccggca actcgccctc	300
atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcatc	420
ctcaccgccc acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag	540
tgggccgact accgggccct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
atcggggaga agacggcgct caagcttctg aaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720

ctgaagctct cctgggacct ggccaagggtg cgcaccgacc tgccccctgga ggtggacttc	780
gccaaaaggc gggagcccgga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg ggaggggaga agccccggga ggaggcccc	900
tggcccccg cggaaagggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta cttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg	1440
ggccaccct tcaacctcaa ctcccgggac cagctggaaa ggggtgctctt tgacgagctt	1500
aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccg gaggacgggc	1680
cgcctccaca ccgcttcaa ccagacggc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggccc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc	1920
cacaccacaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg	1980
cgcggggcgg ccaagacggt gaacttcggc gtccctctac gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttccccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc	2160
tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag	2220
agcgtcaggg aggcgcggga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccg	2340
atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag	2400
gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag	2460
gtggagggtg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac	2520

<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
 195 200 205

Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys

690		695		700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly				
705		710		715 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn				
		725	730	735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn				
		740	745	750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val				
		755	760	765
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln				
		770	775	780
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu				
		785	790	795 800
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala				
		805	810	815
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala				
		820	825	830
Lys Gly His His His His His His				
		835	840	

<210> 545

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 545

ggggagaaga cggcgctcag gcttctgaag gagggggga gcctggaagc

50

<210> 546

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 546

gcttccaggc tcccccactc cttcagaagc ttgagcgccg ttttctcccc

50

<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

ctggtcggga cggacgcaa tgagggtgtg aag

33

<210> 548

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 548

gtccgtcccg accagaat

18

<210> 549

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 549
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
atcctataca gagtctccaa catggctgag gtgggaatca ggccggtgtt tgtattcgac 240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtctgag 300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac 420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
acgagggagc agctcatcga catagcgatt ctggctcggga cggacgcaa tgagggtgtg 720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggctcgagaa ggccttggag 960
aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtgggttc 1008

<210> 550

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Ala Asn Glu Gly Val
 225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu

290		295		300
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu				
305		310		315
				320
Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe				
	325		330	335

<210> 551
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 551
 ctggtcggga cggacaggaa tgaggggtgtg aag 33

<210> 552
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 552
 atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
 ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
 cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cttttccgga 180
 atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtgtt tgtattcgac 240
 ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300
 gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
 caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttttaagttac 420
 atgggggattc cttttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
 gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540

ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600
 tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
 acgagggagc agctcatcga catagcgatt ctggtcggga cggacaggaa tgaggggtgtg 720
 aaggggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg 780
 gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
 aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
 aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttc 1008

<210> 553

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu

115	120	125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro		
130	135	140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala		
145	150	155
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu		
165	170	175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys		
180	185	190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile		
195	200	205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln		
210	215	220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val		
225	230	235
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly		
245	250	255
Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val		
260	265	270
Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr		
275	280	285
Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu		
290	295	300
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu		
305	310	315
Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe		
325	330	335

<210> 554

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554

gaaccacctc tcaagcgtgg

20

<210> 555

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 555

acgcttgaga ggtgggttcct ggaggaggcc ccctgg

36

<210> 556

<211> 1011

<212> DNA

<213> Archaeoglobus fulgidus

<400> 556

atgggtgcgg atattggtga cctctttgag aggggaagagg tcgagcttga gtactttctca 60

ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120

cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180

atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtgtt tgtattcgac 240

ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360

caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttaagttac 420

atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480

gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540

ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600

tatgtggatg taaagccgga gataataatt ctggaaaagca acctcaaaag gctgggtttg 660

acgagggagc agctcatcga catagcgatt ctgggtcggga cggactacaa tgagggtgtg 720

aaggggtgtcg gcgtaagaa ggctttgaac tacatcaaga cctacggaga ttttttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag	960
aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtggttctg a	1011

<210> 557

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 557

taatctgtat caggctg

17

<210> 558

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 558

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac

60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc

240

tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc

300

ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag

360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcg

420

atcctcaccg ccgaccgca cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac

480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag

540

cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	eggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggggtgcgc	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcgggg	gccccgaccg	gaggggctta	gggccttcct	ggagagggtg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcagggggc	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgagggg	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgagggggg	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaaagggt	gctctttgac	1500
gagcttaggc	ttccgcctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccacccgagg	1680
acgggccgcc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcaccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggagggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgtcc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgtcc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaggt	gcgggccttg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcataaagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccagg	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400

gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaaggggtca	ccaccaccac	2520
caccac						2526

<210> 559

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 559

atgggtg	atattggtga	cctctttgag	aggggaagagg	tcgagcttga	gtactttctca	60
ggaaagaaaa	ttgccgttga	tgctttcaac	acgctataacc	agttcatctc	gataataaagg	120
cagcctgacg	gtacgccgtt	aaaggactca	cagggcagaa	tcacctctca	cctttccgga	180
atcctataca	gagtctccaa	catggtcgag	gtgggaatca	ggccggtgtt	tgtattcgac	240
ggagagccac	cggagttcaa	gaaggctgaa	attgaggaga	ggaaaaagag	aagggctgag	300
gcagaggaga	tgtggattgc	ggctttgcag	gcaggagata	aggacgcgaa	aaagtatgct	360
caggctgcag	ggaggggttga	cgagtacatt	gttgactccg	caaagacgct	tttaagttac	420
atggggattc	cctttgtcga	tgccccgtct	gaaggagagg	cgcaggctgc	ttacatggca	480
gcaaaaggcg	atgtggagta	cacaggaagc	caggattacg	attctctgct	cttcggaagc	540
ccgagactcg	ccagaaatct	cgcaataacg	ggaaaaagga	agcttcccgg	caaaaatgtc	600
tatgtggatg	taaagccgga	gataataatt	ctggaaagca	acctcaaaag	gctgggtttg	660
acgagggagc	agctcatcga	catagcgatt	ctggtcggga	cggactacaa	tgaggggtgtg	720
aaggggtgtcg	gcgtcaagaa	ggctttgaac	tacatcaaga	cctacggaga	tattttcagg	780
gcactcaagg	ctctgaaagt	aaatattgac	cacgtagagg	agataaggaa	tttcttcctg	840
aatcctcctg	tgactgacga	ctacagaata	gagttcaggg	agcctgactt	tgagaaggcc	900
atcgagttcc	tgtgcgagga	gcacgacttc	agcagggaga	gggtcgagaa	ggccttggag	960
aagctcaaag	ctctgaagtc	aaccagggcc	acgcttgaga	ggtgggttcct	ggaggaggcc	1020
ccctggcccc	cgccggaagg	ggccttcgtg	ggcttcgtcc	tctcccggcc	cgagcccattg	1080
tgggcggagc	ttaaagccct	ggccgcctgc	aggggcggcc	gcgtgcaccg	ggcagcagac	1140
cccttggcgg	ggctaaagga	cctcaaggag	gtccggggcc	tcctcgccaa	ggacctcgcc	1200

gtcttggcct	cgagggaggg	gctagacctc	gtgcccgggg	acgaccccat	gctcctcgcc	1260
tacctcctgg	acccttcgaa	caccaccccc	gagggggtgg	cgcggcgcta	cgggggggag	1320
tggacggagg	acgccgcca	ccgggccctc	ctctcggaga	ggctccatcg	gaacctcctt	1380
aagcgcctcg	agggggagga	gaagctcctt	tggctctacc	acgaggtgga	aaagcccctc	1440
tcccgggtcc	tggcccatat	ggaggccacc	ggggtacggc	gggacgtggc	ctaccttcag	1500
gccctttccc	tggagcttgc	ggaggagatc	cgccgcctcg	aggaggaggt	cttccgcttg	1560
gcggggccacc	ccttcaacct	caactcccgg	gaccagctgg	aaagggtgct	ctttgacgag	1620
cttaggcttc	ccgccttgaa	gaagacgaag	aagacaggca	agcgctccac	cagcgcccg	1680
gtgctggagg	ccctacggga	ggcccacccc	atcgtggaga	agatcctcca	gcaccgggag	1740
ctcaccaagc	tcaagaacac	ctacgtggac	cccctcccaa	gcctcgtcca	cccgaggacg	1800
ggcgccctcc	acaccgctt	caaccagacg	gccacggcca	cggggagggt	tagtagctcc	1860
gacccaacc	tgcagaacat	ccccgtccgc	acccccttgg	gccagaggat	ccgccgggcc	1920
ttcgtggccg	aggcgggttg	ggcgttggtg	gccctggact	atagccagat	agagctccgc	1980
gtcctcgccc	acctctccgg	ggacgaaaac	ctgatcaggg	tcttccagga	ggggaaggac	2040
atccacaccc	agaccgcaag	ctggatgttc	ggcgtccccc	cggaggccgt	ggaccccctg	2100
atgcgccggg	cggccaagac	ggtgaacttc	ggcgtcctct	acggcatgtc	cgcccatagg	2160
ctctcccagg	agcttgccat	cccctacgag	gaggcggtgg	cctttataga	gcgctacttc	2220
caaagcttcc	ccaaggtg	ggcctggata	gaaaagaccc	tggaggaggg	gaggaagcgg	2280
ggctacgtgg	aaaccctctt	cgaagaagg	cgctacgtgc	ccgacctcaa	cgcccgggtg	2340
aagagcgtca	gggaggccgc	ggagcgc	gccttcaaca	tgcccgcca	gggcaccgcc	2400
gccgacctca	tgaagctcgc	catggtgaag	ctcttcccc	gcctccggga	gatgggggcc	2460
cgcgtgctcc	tccaggctgc	caacgagctc	ctcctggagg	cccccaagc	gcgggccgag	2520
gaggtggcgg	ctttggccaa	ggaggccatg	gagaaggcct	atcccctcgc	cgtgcccctg	2580
gaggtggagg	tggggatggg	ggaggactgg	ctttccgcca	agggtcacca	ccaccaccac	2640
cac						2643

<210> 560

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 370 375 380
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 385 390 395 400
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 435 440 445
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 450 455 460
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 465 470 475 480
 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val

485										490					495				
Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg				
			500					505					510						
Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn				
		515					520					525							
Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro				
	530					535					540								
Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala				
545					550					555					560				
Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu				
				565					570					575					
Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu				
			580					585					590						
Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn				
		595					600					605							
Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu				
	610					615					620								
Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala				
625					630					635					640				
Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln				
				645					650					655					
Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile				
			660					665					670						
Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp				
		675					680					685							
Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala				
	690					695					700								
Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg				
705					710					715					720				
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile				
				725					730					735					

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 770 775 780
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 820 825 830
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 835 840 845
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 850 855 860
 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His
 865 870 875 880

His

<210> 561

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 561

ggttgacttc agagctttga g

21

<210> 562

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 562

aaagctctga agtcaaccct ggaggaggcc ccctgg

36

<210> 563

<211> 2619

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 563

atgggtgctg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca	60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg	120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct tttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaaagca acctcaaaag gctgggtttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cgactacaa tgaggggtgtg	720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgagagga gcacgacttc agcagggaga gggtcgagaa ggccctggag	960
aagctcaaag ctctgaagtc aaccctggag gaggccccct ggcccccgcc ggaaggggccc	1020

ttcgtgggct	tcgtcctctc	ccgccccgag	cccatgtggg	cggagcttaa	agccctggcc	1080
gcctgcaggg	gcggccgcgt	gcaccgggca	gcagacccct	tggcggggct	aaaggacctc	1140
aaggaggtcc	ggggcctcct	cgccaaggac	ctcgccgtct	tggcctcgag	ggaggggcta	1200
gacctcgtgc	ccggggacga	ccccatgctc	ctcgccctacc	tcctggaccc	ttcgaacacc	1260
acccccgagg	gggtggcgcg	gcgctacggg	ggggagtgga	cggaggacgc	cgcccaccgg	1320
gccctcctct	cggagaggct	ccatcggaac	ctccttaagc	gcctcgaggg	ggaggagaag	1380
ctcctttggc	tctaccacga	ggtggaaaag	cccctctccc	gggtcctggc	ccatatggag	1440
gccaccgggg	tacggcgggg	cgtggcctac	cttcaggccc	tttccctgga	gcttgcgagg	1500
gagatccgcc	gcctcgagga	ggaggtcttc	cgttggcggg	gccacccctt	caacctcaac	1560
tcccgggacc	agctggaaaag	ggtgctcttt	gacgagctta	ggcttcccgc	cttgaagaag	1620
acgaagaaga	caggcaagcg	ctccaccagc	gccgcggtgc	tggaggccct	acgggaggcc	1680
caccccatcg	tggagaagat	cctccagcac	cgggagctca	ccaagctcaa	gaacacctac	1740
gtggaccccc	tcccaagcct	cgtccacccg	aggacggggc	gcctccacac	ccgcttcaac	1800
cagacggcca	cggccacggg	gaggcttagt	agctccgacc	ccaacctgca	gaacatcccc	1860
gtccgcaccc	ccttggggcca	gaggatccgc	cgggccttcg	tggccgaggg	gggttgggcg	1920
ttggtggccc	tggactatag	ccagatagag	ctccgcgtcc	tcgcccacct	ctccggggac	1980
gaaaacctga	tcagggtctt	ccaggagggg	aaggacatcc	acaccagac	cgcaagctgg	2040
atgttcggcg	tccccccgga	ggccgtggac	cccctgatgc	gccgggcggc	caagacgggtg	2100
aacttcggcg	tcctctacgg	catgtccgcc	cataggctct	cccaggagct	tgccatcccc	2160
tacgaggagg	cggtaggcctt	tatagagcgc	tacttccaaa	gcttcccaa	ggtgcggggc	2220
tggatagaaa	agaccctgga	ggaggggagg	aagcggggct	acgtggaaac	cctcttcgga	2280
agaaggcgct	acgtgcccga	cctcaacgcc	cgggtgaaga	gcgtcaggga	ggccgcggag	2340
cgcattggcct	tcaacatgcc	cgtccagggc	accgccgccg	acctcatgaa	gctcgccatg	2400
gtgaagctct	tccccgcct	ccgggagatg	ggggcccgcg	tgctcctcca	ggtcgccaac	2460
gagctcctcc	tggaggcccc	ccaagcgcg	gccgaggagg	tggcggcttt	ggccaaggag	2520
gccatggaga	aggcctatcc	cctcgccgtg	cccctggagg	tggagggtggg	gatgggggag	2580
gactggcttt	ccgccaaggg	tcaccaccac	caccaccac			2619

<210> 564

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro
 325 330 335
 Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met
 340 345 350
 Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
 355 360 365
 Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
 370 375 380
 Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
 385 390 395 400
 Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp
 405 410 415
 Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
 420 425 430
 Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
 435 440 445
 Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu
 450 455 460
 Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu

465		470		475		480
Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu						
		485		490		495
Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu						
		500		505		510
Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val						
		515		520		525
Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr						
		530		535		540
Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala						
		545		550		555
His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu						
		565		570		575
Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr						
		580		585		590
Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg						
		595		600		605
Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro						
		610		615		620
Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala						
		625		630		635
Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His						
		645		650		655
Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp						
		660		665		670
Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala						
		675		680		685
Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val						
		690		695		700
Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro						
		705		710		715
						720

Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro
725 730 735

Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg
740 745 750

Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu
755 760 765

Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe
770 775 780

Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met
785 790 795 800

Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu
805 810 815

Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu
820 825 830

Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu
835 840 845

Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser
850 855 860

Ala Lys Gly His His His His His His
865 870

<210> 565

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 565

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60

ggaaagaaaa ttgccgttga tgctttcaac acgctataacc agttcatctc gataataagg 120

cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180

atcctataca gagtctccaa catgggtcgag gtgggaatca ggccggtgtt tgtattcgac 240

ggagagccac	cggagttcaa	gaaggctgaa	attgaggaga	ggaaaaagag	aagggtgag	300
gcagaggaga	tgtggattgc	ggctttgcag	gcaggagata	aggacgcgaa	aaagtatgct	360
caggctgcag	ggagggttga	cgagtacatt	gttgactccg	caaagacgct	tttaagttac	420
atggggattc	cctttgtcga	tgccccgtct	gaaggagagg	cgcaggctgc	ttacatggca	480
gcaaaaggcg	atgtggagta	cacaggaagc	caggattacg	attctctgct	cttcggaagc	540
ccgagactcg	ccagaaatct	cgcaataacg	ggaaaaagga	agcttcccgg	caaaaatgtc	600
tatgtggatg	taaagccgga	gataataatt	ctggaaagca	acctcaaaag	gctgggtttg	660
acgagggagc	agctcatcga	catagcgatt	ctggtcggga	cggactacaa	tgagggtgtg	720
aagggtgtcg	gcgtcaagaa	ggctttgaac	tacatcaaga	cctacggaga	tattttcagg	780
gcactcaagg	ctctgaaagt	aaatattgac	cacgtagagg	agataaggaa	tttcttcctg	840
aatcctcctg	tgactgacga	ctacagaata	gagttcaggg	agcctgactt	tgagaaggcc	900
atcgagttcc	tgtgcgagga	gcacgacttc	agcagggaga	gggtcgagaa	ggccttggag	960
aagctcaaag	ctctgaagtc	aaccagggcc	acgcttgaga	ggtggttcct	ggaggaggcc	1020
ccctggcccc	cgccggaagg	ggccttcgtg	ggcttcgtcc	tctccgccc	cgagcccattg	1080
tgggcgggagc	ttaaagccct	ggccgcctgc	aggggcggcc	gcgtccaccg	ggcccccgag	1140
ccttataaag	ccctcaggga	cctgaaggag	gcgcgggggc	ttctcgccaa	agacctgagc	1200
gttctggccc	tgagggaagg	ccttggcctc	ccgcccggcg	acgaccccat	gctcctcgcc	1260
tacctcctgg	acccttcgaa	caccaccccc	gagggggtgg	cccggcgcta	cggcggggag	1320
tggacggagg	aggcggggga	gcgggcccgc	ctttccgaga	ggctcttcgc	caacctgctt	1380
aagaggcttg	agggggagga	gaggctcctt	tggctttacc	gggaggtgga	gaggcccctt	1440
tccgctgtcc	tggcccatat	ggaggccacg	gggggtgcgc	tggacgtggc	ctatctcagg	1500
gccttgtccc	tggaggtggc	cgaggagatc	gcccgcctcg	aggccgaggt	cttccgcctg	1560
gccggccacc	ccttcaacct	caactcccgg	gaccagctgg	aaagggtcct	ctttgacgag	1620
ctagggcttc	ccgccatcaa	gaagacgcaa	aagaccggca	agcgctccac	cagcgccgcc	1680
gtcctggagg	ccctccgcga	ggcccacccc	atcgtggaga	agatcctgca	gtaccgggag	1740
ctcaccaagc	tgaagagcac	ctacattgac	cccttgccgg	acctcatcca	ccccaggacg	1800
ggccgcctcc	acacccgctt	caaccagacg	gccacggcca	cgggcaggct	aagtagctcc	1860
gatcccaacc	tccagaacat	ccccgtccgc	accccgcttg	ggcagaggat	ccgccgggcc	1920
ttcatcgccg	aggaggggtg	gctattggtg	gccctggact	atagccagat	agagctcagg	1980
gtgctggccc	acctctccgg	cgacgagaac	ctgatccggg	tcttccagga	ggggcgggac	2040
atccacacgg	agaccgccag	ctggatgttc	ggcgtccccc	gggaggccgt	ggaccccctg	2100

atgcgcggg cgccaagac catcaacttc ggggtcctct acggcatgtc ggcccaccgc 2160
 ctctcccagg agctagccat cccttacgag gagggccagg ccttcattga gcgctacttt 2220
 cagagcttcc ccaaggtgcg ggcttgatt gagaagaccc tggaggaggg caggaggcgg 2280
 gggtagctgg agaccctctt cgcccgccgc cgctacgtgc cagacctaga ggcccgggtg 2340
 aagagcgtgc gggaggcggc cgagcgcgtg gccttcaaca tgcccgtcca gggcaccgcc 2400
 gccgacctca tgaagctggc tatggtgaag ctcttcccca ggctggagga aatggggggc 2460
 aggatgctcc ttcaggtcgc caacgagctg gtcctcgagg ccccaaaaga gagggcggag 2520
 gccgtggccc ggctggccaa ggaggtcatg gaggggggtg atcccctggc cgtgcccctg 2580
 gaggtggagg tggggatagg ggaggactgg ctctccgcca aggagcacca ccaccaccac 2640
 cac 2643

<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly

100					105					110					
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
		115					120					125			
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro
	130					135					140				
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
145					150					155					160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu
				165					170					175	
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys
			180					185					190		
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile
		195					200					205			
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln
	210					215					220				
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val
225					230					235					240
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly
				245					250					255	
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val
			260					265					270		
Glu	Glu	Ile	Arg	Asn	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asp	Tyr
		275					280					285			
Arg	Ile	Glu	Phe	Arg	Glu	Pro	Asp	Phe	Glu	Lys	Ala	Ile	Glu	Phe	Leu
	290					295					300				
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu
305					310					315					320
Lys	Leu	Lys	Ala	Leu	Lys	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Arg	Trp	Phe
				325					330					335	
Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe
			340					345					350		

Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
355 360 365
Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
370 375 380
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
385 390 395 400
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
405 410 415
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
420 425 430
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
435 440 445
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Leu Lys Arg Leu Glu
450 455 460
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
465 470 475 480
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
485 490 495
Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
500 505 510
Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
515 520 525
Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
530 535 540
Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
545 550 555 560
Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
565 570 575
Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
580 585 590
Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
595 600 605

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640

Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670

Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 675 680 685

Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700

Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 725 730 735

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750

Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765

Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 805 810 815

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Val Leu
 820 825 830

Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 835 840 845

Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val

850

855

860

Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His
 865 870 875 880

His

<210> 567

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 567

```

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca      60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataaagg      120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga      180
atcctataca gagtctccaa catggctcag gtgggaatca ggccggtggt tgtattcgac      240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag      300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct      360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac      420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca      480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc      540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc      600
tatgtggatg taaagccgga gataataatt ctggaaaagca acctcaaaag gctgggtttg      660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg      720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg      780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg      840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc      900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag      960
aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtggttcct ggaggaggcc     1020
ccctggcccc cgccggaagg ggccttcgtg ggcttcgtcc tctcccgcc cgagcccatg     1080

```

tgggcgagc	ttaaagccct	ggccgcctgc	aggggcggcc	gcgtccaccg	ggccccgag	1140
ccttataaag	ccctcaggga	cctgaaggag	gcgcgggggc	ttctcgccaa	agacctgagc	1200
gttctggccc	tgagggaagg	ccttggcctc	ccgcccggcg	acgaccccat	gctcctcgcc	1260
tacctcctgg	acccttcgaa	caccaccccc	gagggggtgg	cccggcgcta	cggcggggag	1320
tggacggagg	aggcggggga	gcggggccgc	ctttccgaga	ggctcttcgc	caacctgtgg	1380
gggaggcttg	agggggagga	gaggctcctt	tggctttacc	gggagggtga	gaggcccctt	1440
tccgctgtcc	tggcccatat	ggaggccacg	gggggtgcgc	tggacgtggc	ctatctcagg	1500
gccttgctcc	tggagggtgg	cgaggagatc	gcccgcctcg	aggccgaggt	cttcgcctg	1560
gccggccacc	ccttcaacct	caactcccgg	gaccagctgg	aaagggtcct	ctttgacgag	1620
ctagggcttc	ccgccatcgg	caagacggag	aagaccggca	agcgctccac	cagcgccgcc	1680
gtcctggagg	ccctccgcga	ggccaccccc	atcgtggaga	agatcctgca	gtaccgggag	1740
ctcaccaagc	tgaagagcac	ctacattgac	cccttgccgg	acctcatcca	ccccaggacg	1800
ggccgcctcc	acacccgctt	caaccagacg	gccacggcca	cgggcaggct	aagtagctcc	1860
gatcccaacc	tccagaacat	ccccgtccgc	accccgcttg	ggcagaggat	ccgccggggc	1920
ttcatcgccg	aggaggggtg	gctattgggtg	gccctggact	atagccagat	agagctcagg	1980
gtgctggccc	acctctccgg	cgacgagaac	ctgatccggg	tcttccagga	ggggcgggac	2040
atccacacgg	agaccgccag	ctggatgttc	ggcgtccccc	gggaggccgt	ggaccccctg	2100
atgcgccggg	cggccaagac	catcaacttc	ggggtcctct	acggcatgtc	ggccccaccg	2160
ctctcccagg	agctagccat	cccttacgag	gaggcccagg	ccttcattga	gcgctacttt	2220
cagagcttcc	ccaagggtgcg	ggcctggatt	gagaagacct	tggaggaggg	caggaggcgg	2280
gggtacgtgg	agaccctctt	cggccgccgc	cgctacgtgc	cagacctaga	ggcccgggtg	2340
aagagcgtgc	gggaggcggc	cgagcgcgtg	gccttcaaca	tgcccgtcca	gggcaccgcc	2400
gccgacctca	tgaagctggc	tatggtgaag	ctcttcccca	ggctggagga	aatggggggc	2460
aggatgctcc	ttcagggtcca	caacgagctg	gtcctcgagg	ccccaaaaga	gagggcgagg	2520
gccgtggccc	ggctggccaa	ggagggtcatg	gaggggggtg	atcccctggc	cgtgcccctg	2580
gagggtggagg	tggggatagg	ggaggactgg	ctctccgccca	aggagcacca	ccaccaccac	2640
cac						2643

<210> 568

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350

Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365

Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380

Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400

Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415

Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430

Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445

Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
 450 455 460

Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu

465		470		475		480									
Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	Leu	Asp	Val
				485					490					495	
Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	Glu	Ile	Ala	Arg
			500					505					510		
Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn
		515					520					525			
Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Gly	Leu	Pro
	530					535					540				
Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala
545					550					555					560
Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu
				565					570					575	
Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Pro	Leu
			580					585					590		
Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn
		595					600					605			
Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu
		610				615						620			
Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala
625					630					635					640
Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln
				645					650					655	
Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile
			660					665					670		
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp
		675					680					685			
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
	690					695					700				
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
705					710					715					720

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
725 730 735

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
740 745 750

Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
755 760 765

Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
785 790 795 800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
805 810 815

Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asn Glu Leu Val Leu
820 825 830

Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
835 840 845

Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
850 855 860

Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His
865 870 875 880

His

<210> 569

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

gagcggataa caatttcaca cagg

24

<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

tgcccgggtgc acgcggccgc ccctgcaggc

30

<210> 571

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

atgaattccc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggccctacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggcccc tccttccgcc accagacctt cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcac cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcacccacg tcctccaccc cgaggggtac	480
ctcatcacc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccac	540
taccgggccc tgaccgggga cgagtccgac aaccttcccg ggggtcaagg catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccg accgggaggg ggagaagccc cgggaggagg ccccttgccc cccgcccga	840
ggggccttcg tgggcttcct cctttccgc cccgagccca tgtgggcgga gcttaaagcc	900

ctggccgcct gcaggggcg	ccgcgtgcac cgggcagcag	accccttggc ggggctaaag	960
gacctcaagg aggtccggg	cctcctcgcc aaggacctcg	ccgtcttggc ctcgagggag	1020
gggctagacc tcgtgcccgg	ggacgacccc atgctcctcg	cctacctcct ggacccttcg	1080
aacaccaccc ccgaggggg	ggcgcgggcg tacggggggg	agtggacgga ggacgccgcc	1140
caccggggccc tcctctcgga	gaggctccat cggaacctcc	ttaagcgctc cgagggggag	1200
gagaagctcc tttggctcta	ccacgaggtg gaaaagcccc	tctcccgggt cctggcccat	1260
atggaggcca ccggggtacg	gcgggacgtg gcctaccttc	aggccctttc cctggagctt	1320
gcgaggagga tccgccgcct	cgaggaggag gtcttccgct	tggcggggcca ccccttcaac	1380
ctcaactccc gggaccagct	ggaaaggggt ctctttgacg	agcttaggct tcccgcttg	1440
aagaagacga agaagacagg	caagcgctcc accagcgccg	cgggtgctgga ggccctacgg	1500
gaggccacc ccatcgtgga	gaagatcctc cagcaccggg	agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc	aagcctcgtc caccgagga	cgggccgcct ccacaccgc	1620
ttcaaccaga cggccacggc	cacggggagg cttagtagct	ccgaccccaa cctgcagaac	1680
atccccgtcc gcaccccctt	gggccagagg atccgccggg	ccttcgtggc cgaggcgggt	1740
tgggcgttgg tggccctgga	ctatagccag atagagctcc	gcgtcctcgc ccacctctcc	1800
ggggacgaaa acctgatcag	ggtcttccag gagggaagg	acatccacac ccagaccgca	1860
agctggatgt tcggcgctcc	cccggaggcc gtggaccccc	tgatgcgccg ggcggccaag	1920
acggtgaact tcggcgctcc	ctacggcatg tccgcccata	ggctctccca ggagcttgcc	1980
atccccctacg aggaggcgg	ggcctttata gagcgctact	tccaaagctt cccaagggtg	2040
cgggcctgga tagaaaagac	cctggaggag gggaggaagc	ggggctacgt ggaaaccctc	2100
ttcggaagaa ggcgctacgt	gcccgcctc aacgcccggg	tgaagagcgt caggagggcc	2160
gcggagcgca tggccttcaa	catgcccgtc cagggcaccg	ccgccgacct catgaagctc	2220
gccatggtga agctcttccc	ccgcctccgg gagatggggg	cccgcacgtc cctccaggtc	2280
gccaacgagc tcctcctgga	ggccccccaa gcgcggggccg	aggaggtggc ggctttggcc	2340
aaggaggcca tggagaaggc	ctatcccctc gccgtgcccc	tggaggtgga ggtggggatg	2400
ggggaggact ggctttccgc	caagggtcac caccaccacc	accac	2445

<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350

Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp

	725		730		735
Leu Met Lys	Leu Ala Met Val Lys	Leu Phe Pro Arg	Leu Arg Glu Met		
	740	745	750		
Gly Ala Arg	Met Leu Leu Gln Val Ala Asn Glu	Leu Leu Leu Glu Ala			
	755	760	765		
Pro Gln Ala	Arg Ala Glu Glu Val Ala Ala Leu	Ala Lys Glu Ala Met			
	770	775	780		
Glu Lys Ala Tyr	Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met				
	785	790	795	800	
Gly Glu Asp Trp	Leu Ser Ala Lys Gly His His His His His His				
	805	810	815		

<210> 573

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 573

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgcga cgaggcctac	240
gggggggtaca aggcggggccg ggccccacc ccggaggact tccccgcga gctcgccttg	300
gtcaagcggc tggtagacct tctgggcctg gtccgcctcg agggcccggt gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
ctcaccgcgc accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
tgggtggact accgggcctt ggccggggac ccttcgcga acatcccccg cgtgaagggc	600
atcggggaga agacggcggc caagctgac cgggagtggg gaagcctgga aaacctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720

ctgaagctct cctgggacct ggccaagggtg cgcaccgacc tgccccctgga ggtggacttc	780
gccaaaaggc gggagcccgga ccgggagagg cttagggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg gaaagcccca aggccctgga ggaggccccc	900
tggcccccg cgggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg	960
gcggagctta aagccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gcccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg	1440
ggccaccct tcaacctcaa ctcccgggac cagctggaaa ggggtgctct tgacgagctt	1500
aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccg gaggacgggc	1680
cgcctccaca ccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggcc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc	1920
cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg	1980
cgcggggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc	2160
tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag	2220
agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccg	2340
atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag	2400
gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag	2460
gtggagggtg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac	2520

<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
50 55 60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg
100 105 110

Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140

Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175

Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
180 185 190

Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
 195 200 205

Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
 210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys

690	695	700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly		
705	710	715 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn		
	725	730 735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn		
	740	745 750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val		
	755	760 765
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln		
	770	775 780
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu		
	785	790 795 800
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala		
	805	810 815
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala		
	820	825 830
Lys Gly His His His His His His		
	835	840

<210> 575

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

atgaattccc tgcccctcctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acggggtttgc caagagcctt ttgaaggcgc taaggggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcc accagacctt cgaggcctac	240

aaggcggggc	gggctccac	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggctt	taccgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaag	gagggctacg	aggtccgcat	cctcaccgcc	420
gacaaagacc	tttaccagct	cctttccgac	cgcattccacg	tcctccaccc	cgaggggtac	480
ctcatcacc	cggcctggct	ttgggaaaag	tacggcctga	ggcccgacca	gtgggcccgc	540
taccgggccc	tgaccgggga	cgagtccgac	aaccttccc	gggtcaaggg	catcggggag	600
aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
gaccggctga	agcccgccat	ccgggagaag	atcctggccc	acatggacga	tctgaagctc	720
tcctgggacc	tggccaaggt	gcgcaccgac	ctgcccctgg	aggtggactt	cgccaaaagg	780
cgggagcccc	accgggaggg	ggagaagccc	cgggagggag	ccccctggcc	cccggccgaa	840
ggggccttcg	tgggcttct	cctttcccgc	cccagaccca	tgtgggcgga	gcttaaagcc	900
ctggccgcct	gcaggggagg	ccgcgtgcac	cgggcagcag	accttggc	ggggctaaag	960
gacctcaagg	aggtccgggg	cctcctcgcc	aaggacctcg	ccgtcttggc	ctcgagggag	1020
gggctagacc	tcgtgcccg	ggacgacccc	atgctcctcg	cctacctcct	ggacccttcg	1080
aacaccaccc	ccgagggggg	ggcgcggcgc	tacggggggg	agtggacgga	ggacgccgcc	1140
caccgggccc	tcctctcgga	gaggctccat	cggaacctcc	ttaagcgct	cgagggggag	1200
gagaagctcc	tttggctcta	ccacgagggtg	gaaaagcccc	tctccgggt	cctggcccat	1260
atggaggcca	ccgggggtacg	gcgggacgtg	gcctaccttc	aggccctttc	cctggagctt	1320
gcggaggaga	tccgccgcct	cgaggaggag	gtcttccgct	tggcgggcca	ccccttcaac	1380
ctcaactccc	gggaccagct	ggaaagggtg	ctctttgacg	agcttaggct	tcccgcttg	1440
aagaagacga	agaagacagg	caagcgctcc	accagcgccg	cggtgctgga	ggccctacgg	1500
gaggcccacc	ccatcgtgga	gaagatcctc	cagcaccggg	agctcaccaa	gctcaagaac	1560
acctacgtgg	acccctccc	aagcctcgtc	caccgagga	cgggccgcct	ccacaccgc	1620
ttcaaccaga	cggccacggc	cacggggagg	cttagtagct	ccgaccccaa	cctgcagaac	1680
atccccgtcc	gcacccctt	gggacagagg	atccgccggg	ccttcgtggc	cgaggcgggt	1740
tgggcgttgg	tggccctgga	ctatagccag	atagagctcc	gcgtcctcgc	ccacctctcc	1800
ggggacgaaa	acctgatcag	ggtcttccag	gaggggaagg	acatccacac	ccagaccgca	1860
agctggatgt	tcggcgtccc	cccggaggcc	gtggaccccc	tgatgcgccg	ggcggccaag	1920
acggtgaact	tcggcgtcct	ctacggcatg	tccgcccata	ggctctccca	ggagcttgcc	1980
atccccctacg	aggaggcgggt	ggcctttata	gagcgctact	tccaaagctt	ccccaaagggtg	2040
cgggcctgga	tagaaaagac	cctggaggag	gggaggaagc	ggggctacgt	ggaaaccctc	2100

ttcggaagaa ggcgctacgt gcccgcacctc aacgcccggg tgaagagcgt cagggaggcc 2160
 gcggagcgca tggccttcaa catgcccgtc cagggcacccg ccgcccacct catgaagctc 2220
 gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc 2280
 gccaacgagc tcctcctgga ggccccccaa gcgcggggccg aggaggtggc ggctttggcc 2340
 aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtgggggatg 2400
 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
 1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu

130		135		140
Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr				
145		150		155 160
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp				
	165		170	175
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu				
	180		185	190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu				
	195		200	205
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys				
	210		215	220
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu				
	225		230 235	240
Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp				
	245		250	255
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu				
	260		265	270
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu				
	275		280	285
Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys				
	290		295	300
Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys				
	305		310	315 320
Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu				
		325	330	335
Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu				
	340		345	350
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala				
	355		360	365
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu				
	370		375	380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
660 665 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
675 680 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac

60

ggccaccacc	tggcctaccg	cacctttcttc	gccctgaagg	gcctcaccac	gagccggggc	120
gaaccggtgc	aggcggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	caaggaggac	180
ggggacgcgg	tgatcgtggt	ctttgacgcc	aaggccccct	ccttcgccca	cgaggcctac	240
gggggggtaca	aggcggggccg	ggccccacc	ccggaggact	tccccgccca	gctcgccttg	300
gtcaagcggc	tggtggacct	tctgggcttt	accgcctcg	aggccccggg	gtacgaggcg	360
gacgacgtcc	tgggcaccct	ggccaagaag	gccgaaaagg	aggggtacga	ggtgcgcatac	420
ctcaccgccg	accgcgacct	ctaccaactc	gtctccgacc	gcatccacgt	cctccacccc	480
gaggggtacc	tcatcacccc	ggagtggctt	tgggagaagt	atgggcttaa	gccttcccag	540
tgggtggact	accgggcctt	ggccggggac	ccttcgcaca	acatccccgg	cgtgaagggc	600
atcggggaga	agacggcggc	caagctgata	cgggagtggg	gaagcctgga	aaacctcctc	660
aagaacctgg	accggctgaa	gccccccatc	cgggagaaga	tcctggccca	catggacgat	720
ctgaagctct	cctgggacct	ggccaagggt	cgcaccgacc	tgccccgga	ggtggacttc	780
gccaaaaggc	gggagcccga	ccgggagagg	cttagggcct	ttctggagag	gcttgagttt	840
ggcagcctcc	tccacgagtt	cggccttctg	gaaagcccca	aggccctgga	ggaggccccc	900
tggccccccg	cggaaggggc	cttcgtgggc	ttcgtcctct	cccgccccga	gcccattgtg	960
gcggagctta	aagccctggc	cgcctgcagg	ggcggccgcg	tgcaccgggc	agcagacccc	1020
ttggcggggc	taaaggacct	caaggaggtc	cggggcctcc	tcgccaagga	cctcgccgtc	1080
ttggcctcga	gggaggggct	agacctcgtg	cccggggacg	accccatgct	cctcgcctac	1140
ctcctggacc	cttcgaacac	cacccccgag	ggggtggcgc	ggcgctacgg	gggggagtg	1200
acggaggacg	ccgcccaccg	ggccctcctc	tcggagaggc	tccatcgga	cctccttaag	1260
cgcctcgagg	gggaggagaa	gctccttttg	ctctaccacg	aggtggaaaa	gcccctctcc	1320
cgggtcctgg	cccatatgga	ggccaccggg	gtacggcggg	acgtggccta	ccttcaggcc	1380
ctttccctgg	agcttgcgga	ggagatccgc	cgcctcgagg	aggaggctct	ccgcttggcg	1440
ggccacccct	tcaacctcaa	ctcccgggac	cagctggaaa	gggtgctctt	tgacgagctt	1500
aggcttcccc	ccttgaagaa	gacgaagaag	acaggcaagc	gctccaccag	cgccgcggtg	1560
ctggaggccc	tacgggaggc	ccaccccatc	gtggagaaga	tcctccagca	ccgggagctc	1620
accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttgggcc	agaggatccg	ccgggccttc	1800
gtggccgagg	cgggttgggc	gttgggtggc	ctggactata	gccagataga	gctccgcgtc	1860
ctcgcccacc	tctccgggga	cgaaaacctg	atcagggctc	tccaggaggg	gaaggacatc	1920

cacacccaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg 1980
 cgccggggcgg ccaagacggt gaacttcggc gtccctctacg gcatgtccgc ccataggctc 2040
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160
 tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccgc 2340
 atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
 50 55 60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
 65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
 85 90 95

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg

100	105	110
Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala		
115	120	125
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp		
130	135	140
Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro		
145	150	155
Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu		
	165	170
Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser		
	180	185
Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys		
	195	200
Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp		
	210	215
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp		
225	230	235
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu		
	245	250
Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg		
	260	265
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly		
	275	280
Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro		
	290	295
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp		
305	310	315
Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg		
	325	330
Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly		
	340	345
		350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620
Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625 630 635 640
His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
645 650 655
Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670
Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
675 680 685
Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
690 695 700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705 710 715 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
725 730 735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830
Lys Gly His His His His His His
835 840

<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

atgaattccc	tgcccctctt	tgagcccaag	ggccgggtgc	ttctggtgga	cggccaccac	60
ctggcctacc	gtaccttttt	tgccctgaag	ggcctcacca	ccagccgcgg	ggagccggtc	120
caggcgggtg	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
gtgatcgtgg	tctttgacgc	cgaggccccc	tccttcgcgc	accagacctt	cgaggcctac	240
aaggcggggc	gggctccccc	ccccgaggac	ttcccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggcct	ggagcgccct	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtccgcac	cctcaccgcc	420
gacaaagacc	tttaccagct	cctttccgac	cgcattccacg	tcctccaccc	cgaggggtac	480
ctcatcacc	cggcctggct	ttgggaaaag	tacggcctga	ggcccgaaca	gtgggcccgc	540
taccgggccc	tgaccgggga	cgagtccgac	aaccttcccc	gggtcaaggg	catcggggag	600
aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
gaccggctga	agcccgccat	ccggggagaag	atcctggccc	acatggacga	tctgaagctc	720
tcctgggacc	tggccaaggt	gcgcaccgac	ctgcccctgg	aggtggactt	cgccaaaagg	780
cgggagcccc	accgggaggg	ggagaagccc	cgggaggagg	ccccctggcc	cccggccgaa	840
ggggccttcg	tgggcttcct	cctttccgcg	cccagagcca	tgtgggcgga	gcttaaagcc	900
ctggccgcct	gcagggggcg	ccgcgtgcac	cgggcagcag	acctcttggc	ggggctaaaag	960
gacctcaagg	aggtccgggg	cctcctcgcc	aaggacctcg	ccgtcttggc	ctcgagggag	1020
gggctagacc	tcgtgcccgg	ggacgacccc	atgctcctcg	cctacctcct	ggacccttcg	1080
aacaccaccc	ccgagggggg	ggcgcgccgc	tacggggggg	agtggacgga	ggacgcccgc	1140
caccgggccc	tcctctcgga	gaggctccat	cggaacctcc	ttaagcgcc	cgagggggag	1200
gagaagctcc	tttggtctta	ccacgaggtg	gaaaagcccc	tctcccgggt	cctggcccat	1260
atggaggcca	ccgggggtacg	gcgggacgtg	gcctaccttc	aggccctttc	cctggagctt	1320
gcggaggaga	tcgcgcgcct	cgaggaggag	gtcttcgcgt	tggcgggcca	ccccttcaac	1380
ctcaactccc	gggaccagct	ggaaaggggt	ctctttgacg	agcttaggct	tcccgccctg	1440
aagaagacga	agaagacagg	caagcgctcc	accagcgccg	cgggtgctgga	ggccctacgg	1500

gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac 1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggcccgcct ccacacccgc 1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac 1680
atccccgtcc gcacccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt 1740
tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc 1800
ggggacgaaa acctgatcag ggtcttcag gaggggaagg acatccacac ccagaccgca 1860
agctggatgt tcggcgtccc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag 1920
acggtgaact tcggcgtcct ctacggcatg tccgcccata ggctctccca ggagcttgcc 1980
atccccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt cccaagggtg 2040
cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc 2100
ttcggaagaa ggcgtacgt gcccgaacct aacgcccggg tgaagagcgt cagggaggcc 2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc 2280
gccaacgagc tcctcctgga ggccccccaa gcgcggggcc aggaggtggc ggctttggcc 2340
aaggaggcca tggagaaggc ctatccccct gccgtgcccc tggaggtgga ggtggggatg 2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10				15		

Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			

Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50		55		60											
Phe 65	Asp	Ala	Glu	Ala	Pro 70	Ser	Phe	Arg	His	Gln 75	Thr	Tyr	Glu	Ala	Tyr 80
Lys	Ala	Gly	Arg	Ala 85	Pro	Thr	Pro	Glu	Asp 90	Phe	Pro	Arg	Gln	Leu 95	Ala
Leu	Ile	Lys	Glu 100	Met	Val	Asp	Leu	Leu 105	Gly	Leu	Glu	Arg	Leu 110	Glu	Val
Pro	Gly	Phe 115	Glu	Ala	Asp	Asp	Val 120	Leu	Ala	Thr	Leu	Ala 125	Lys	Lys	Ala
Glu	Lys 130	Glu	Gly	Tyr	Glu	Val 135	Arg	Ile	Leu	Thr	Ala 140	Asp	Lys	Asp	Leu
Tyr 145	Gln	Leu	Leu	Ser	Asp 150	Arg	Ile	His	Val	Leu 155	His	Pro	Glu	Gly	Tyr 160
Leu	Ile	Thr	Pro	Ala 165	Trp	Leu	Trp	Glu	Lys 170	Tyr	Gly	Leu	Arg	Pro	Asp 175
Gln	Trp	Ala	Asp 180	Tyr	Arg	Ala	Leu	Thr 185	Gly	Asp	Glu	Ser	Asp 190	Asn	Leu
Pro	Gly	Val 195	Lys	Gly	Ile	Gly	Glu 200	Lys	Thr	Ala	Arg	Lys 205	Leu	Leu	Glu
Glu	Trp 210	Gly	Ser	Leu	Glu	Ala 215	Leu	Leu	Lys	Asn	Leu 220	Asp	Arg	Leu	Lys
Pro	Ala 225	Ile	Arg	Glu	Lys 230	Ile	Leu	Ala	His	Met 235	Asp	Asp	Leu	Lys	Leu 240
Ser	Trp	Asp	Leu	Ala 245	Lys	Val	Arg	Thr	Asp 250	Leu	Pro	Leu	Glu	Val 255	Asp
Phe	Ala	Lys	Arg 260	Arg	Glu	Pro	Asp	Arg 265	Glu	Gly	Glu	Lys	Pro 270	Arg	Glu
Glu	Ala	Pro 275	Trp	Pro	Pro	Pro	Glu 280	Gly	Ala	Phe	Val	Gly 285	Phe	Leu	Leu
Ser	Arg 290	Pro	Glu	Pro	Met	Trp 295	Ala	Glu	Leu	Lys	Ala 300	Leu	Ala	Ala	Cys

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560

Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
565 570 575

Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
580 585 590

Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
595 600 605

Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
610 615 620

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625 630 635 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
660 665 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
675 680 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His

805

810

815

<210> 581

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

```

atgaattccc tgccccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac      60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc      120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac      240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag      300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
ctggctaccc tggccaagaa ggcgaaaag gagggctacg aggtccgcac cctcaccgcc      420
gacaaagacc tttaccagct cctttccgac cgcacccacg tcctccaccc cgaggggtac      480
ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccgc      540
taccggggcc tgaccgggga cgagtccgac aaccttcccg gggtaaggga catcggggag      600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg      660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc      720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg      780
cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga      840
ggggccttcg tgggcttcct cctttccgc cccgagccca tgtgggcgga gcttaaagcc      900
ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag      960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag     1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggacccttcg     1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgccgcc     1140
caccgggccc tcctctcgga gaggtcccat cggaacctcc ttaagcgctt cgagggggag     1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccggtt cctggcccat     1260
atggaggcca ccggggtacg gcgggacgtg gcctaccttc aggccctttc cctggagctt     1320

```

gcggaggaga tccgccgcct cgaggaggag gtcttccgct tggcgggcca ccccttcaac 1380
ctcaactccc gggaccagct ggaaaggggtg ctctttgacg agcttaggct tcccgccttg 1440
aagaagacga agaagacagg caagcgctcc accagcgccg cggtgctgga ggccctacgg 1500
gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac 1560
acctacgtgg accccctccc aagcctcgtc cacccgagga cgggcccgcct ccacacccgc 1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac 1680
atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt 1740
tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc 1800
ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca 1860
agctggatgt tcggcgctcc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag 1920
acggtgaact tcggcgctct ctacggcatg tccgcccata ggctctccca ggagcttgcc 1980
atccccctacg aggaggcggg ggcctttata gacgctact tccaaagctt cccaagggtg 2040
cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc 2100
ttcggaagaa ggcgtacgt gcccgcctc aacgcccggg tgaagagcgt cagggaggcc 2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcatgct cctccaggtc 2280
gccaacgagc tcctcctgga ggccccccaa gcgcggggccg aggaggtggc ggctttggcc 2340
aaggaggcca tggagaaggc ctatccccctc gccgtgcccc tggaggtgga ggtggggatg 2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	

Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60
 Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350

Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495

Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510

Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525

Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr

530					535					540					
Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn
545					550					555					560
Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val
				565					570					575	
Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu
			580					585					590		
Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val
		595					600					605			
Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe
	610					615					620				
Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys
625					630					635					640
Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser
				645					650					655	
Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg
			660					665					670		
Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu
		675				680						685			
Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg
	690					695					700				
Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala
705					710					715					720
Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp
				725					730					735	
Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met
			740					745					750		
Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala
		755					760					765			
Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met
				770			775				780				

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg tacctttttt gccctgaagg gcctcaccac cagccggggg	120
gagccgggtcc aggcgggtgta cgggtttgcc aagagccttt tgaaggcgct aagagaagac	180
ggggacgcgg tgatcgtggt ctttgacgcc gaggccccct ccttccgcca cgaggcctac	240
gggggggtaca aggcggggcg ggctcccaacc cccgaggact ttccccggca gcttgccctt	300
atcaaggagc tgggtggacct cctgggggttt accgcctcgc aggtcccccg ctacgaggcg	360
gacgacgttc tcgccaccct ggccaagaag gcggaaaagg aggggtacga ggtgcgcac	420
ctcaccgcgc acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggttt tgggaaaagt acggcctgag gcccgaccag	540
tgggccgact accgggccct gaccggggac gaggccgaca accttcccgc ggtcaagggc	600
atcggggaga agaccgccct caagctcctc aaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgccccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttttggagag gctggagttc	840
ggcagcctcc tcacagagtt cggcctcctg ggaggggaga agccccggga ggaggcccc	900
tggccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg	1200

acggaggacg cgcgccaccg ggccctctctc tcggagaggc tccatcggaa cctccttaag 1260
 cgcctcgagg gggaggagaa gctccttttg ctctaccacg aggtggaaaa gcccctctcc 1320
 cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc 1380
 ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg 1440
 ggccacccct tcaacctcaa ctcccgggac cagctggaaa ggggtgctctt tgacgagctt 1500
 aggttccccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg 1560
 ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc 1620
 accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc 1680
 cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740
 cccaacctgc agaacatccc cgtccgcacc cccttggggc agaggatccg ccgggccttc 1800
 gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgctc 1860
 ctgcgccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc 1920
 cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg 1980
 cgccgggcgg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc 2040
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100
 agcttcccca aggtgcgggc ctggatagaa aagacctgg aggaggggag gaagcggggc 2160
 tacgtgaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccg 2340
 atgtctctcc aggtcgccaa cgagctctct ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggagggtg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val

1	5	10	15
Leu Leu Val	Asp Gly His His	Leu Ala Tyr Arg Thr Phe	Phe Ala Leu
	20	25	30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly	35	40	45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val	50	55	60
Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr	65	70	75
Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg	85	90	95
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg	100	105	110
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala	115	120	125
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	130	135	140
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	145	150	155
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	165	170	175
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	180	185	190
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys	195	200	205
Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp	210	215	220
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp	225	230	235
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu	245	250	255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val

755		760		765											
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
770						775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795				800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		
Lys	Gly	His	His	His	His	His	His								
		835					840								

<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585

atgaattccc	tgccccctctt	tgagcccaag	agccgggtgc	ttctggtgga	cggccaccac	60
ctggcctacc	gcacctcctt	cgccctgaag	ggcctcacca	ccagccgcgg	ggagccggtg	120
cagatggtct	acggcttcgc	ccggagcctc	ctcaaggcct	tgaaggagga	cggacaggcg	180
gtggtcgtgg	tctttgacgc	caaggccccc	tccttcgcgc	acgaggccta	cgaggcctac	240
aaggcggggc	gggccccccac	cccggaggac	ttccccggca	gctcgccctt	atcaaggaga	300
tggtggacct	tttgggcctg	gcgcgcctcg	aggtcccggg	ctacgaggcg	gacgacgttc	360
tcgccaccct	ggccaagaag	gcggaaaagg	aggggtacga	ggtgcgcatt	ctaccgccga	420
ccgcgacctc	taccaactcg	tctccgaccg	cgtcgccgtc	ctccaccccc	agggccacct	480
catcaccocg	gagtggcttt	gggagaagta	cggcctcagg	ccggagcagt	gggtggactt	540
ccgcgccttc	gtggggggacc	cctccgacaa	cctccccggg	gtcaagggca	tcgggggagga	600
gacggcggcc	aagctgatcc	gggagtgggg	aagcctggaa	aaccttctta	agcacctgga	660
acaggcgaaa	cctgcctccg	tgcgggagaa	gaccccttagc	cacatggagg	acctcaagct	720

atccctggag ctatcccggg tgcacacgga cttgcttctt cagtggactt taaggccctg	780
cgccgcagga cccccgacct ggagggcctg agggcctttt tggaggagct ggagttcggc	840
agcctcctcc acgagttcgg cctcctggag gccccgcgcg cggcggagga agctccctgg	900
ccgccccccg aggagacctt cgtggggtac gttctttccc gccccgagcc catgtgggcg	960
gagcttaacg ccttggccgc cgctggggc ggccgcgtgc accgggcagc agacccttg	1020
gcggggctaa aggacctcaa ggaggtccgg ggctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgccctacctc	1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgcgc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccctggagc ttgcggagga gatccgcgcg ctcgaggagg aggtcttccg cttggcgggc	1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcggt gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccaccgag gacgggcccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttggggccaga ggatccgccc ggcttctgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaaag tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgcccac	2280
ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg gggccgcatg	2340
ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggagggtg	2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
gagggtgggga tgggggagga ctggccttcc gccaaagggt	2499

<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
145 150 155 160

Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys
165 170 175

Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser
180 185 190

Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg
 195 200 205
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu
 210 215 220
 Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly
 225 230 235 240
 Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu
 245 250 255
 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala
 260 265 270
 Ala Glu Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Tyr
 275 280 285
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala
 290 295 300
 Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 305 310 315 320
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 325 330 335
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 340 345 350
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 355 360 365
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 370 375 380
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 385 390 395 400
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 405 410 415
 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
 420 425 430
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 435 440 445

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 450 455 460
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 465 470 475 480
 Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 675 680 685
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly

690	695	700
Arg Arg Arg Tyr Val	Pro Asp Leu Asn Ala	Arg Val Lys Ser Val Arg
705	710	715 720
Glu Ala Ala Glu Arg	Met Ala Phe Asn Met	Pro Val Gln Gly Thr Ala
	725	730 735
Ala Asp Leu Met Lys	Leu Ala Met Val	Lys Leu Phe Pro Arg Leu Arg
	740	745 750
Glu Met Gly Ala Arg	Met Leu Leu Gln Val	Ala Asn Glu Leu Leu Leu
	755	760 765
Glu Ala Pro Gln Ala	Arg Ala Glu Glu Val	Ala Ala Leu Ala Lys Glu
	770	775 780
Ala Met Glu Lys Ala	Tyr Pro Leu Ala Val	Pro Leu Glu Val Glu Val
	785	790 795 800
Gly Met Gly Glu Asp	Trp Leu Ser Ala	Lys Gly
	805	810

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

atggaattcc tgccccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gcaccttcca cgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cgggggatgtg	180
gtgatcgtgg tctttgacgc caaggccccc tccttccgcc acgaggccta cgggggggtac	240
aaggcggggc gggccccgac ccccgaggac ttcccccggc agctcgccct catcaaggag	300
ctggtggacc tcctggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtgcgcat tctcaccggc	420
gaccgcgacc tttaaccaact cgtctccgac cgcgtcgcca ggccggagca gtgggtggac	480

taccgggcct	tggccgggga	cccttccgac	aacatccccg	gcgtgaaggg	catcggggag	540
aagacggcga	ggaagcttct	ggaggagtgg	gggagcgtgg	aagccctcct	caagaacctg	600
gaccggctga	agccccccat	ccgggagaag	atcctggccc	acatggagga	cctcaagcta	660
tccctggagc	tatcccgggt	gcgcaccgac	ctccccctgg	aggtggacct	cgcccagggg	720
cgggagcccc	accgggaggg	gcttaaggcc	tttttgagga	ggctggagtt	cggaagcctc	780
ctccacgagt	tgggcctgtt	ggaaagcccc	gtggcggcgg	aggaagctcc	ctggccgccc	840
cccaggggag	ccttcgtggg	gtacgttctt	tcccgcctcg	agcccatgtg	ggcggagctt	900
aacgccttgg	ccgccgcctg	gggcggccgc	gtgcaccggg	cagcagaccc	cttggcgggg	960
ctaaaggacc	tcaaggaggt	ccggggcctc	ctcgccaagg	acctcgccgt	cttggcctcg	1020
agggaggggc	tagacctcgt	gcccggggac	gaccccatgc	tcctcgccct	cctcctggac	1080
ccttcgaaca	ccacccccga	gggggtggcg	cggcgctacg	ggggggagtg	gacggaggac	1140
gccgcccacc	gggccctcct	ctcgagaggg	ctccatcgga	acctccttaa	gcgcctcgag	1200
ggggaggaga	agctcctttg	gctctaccac	gaggtggaaa	agccccctct	ccgggtcctg	1260
gcccataatg	aggccaccgg	ggtacggcgg	gacgtggcct	accttcaggc	cctttccctg	1320
gagcttgccg	aggagatccg	ccgcctcgag	gaggaggtct	tccgcttggc	gggccacccc	1380
ttcaacctca	actcccggga	ccagctggaa	aggggtgctct	ttgacgagct	taggcttccc	1440
gccttgaaga	agacgaagaa	gacaggcaag	cgctccacca	gcgccgcggt	gctggaggcc	1500
ctacgggagg	cccaccccat	cgtggagaag	atcctccagc	accgggagct	caccaagctc	1560
aagaacacct	acgtggaccc	cctcccaagc	ctcgtccacc	cgaggacggg	ccgcctccac	1620
acccgcttca	accagacggc	cacggccacg	gggaggctta	gtagctccga	ccccaacctg	1680
cagaacatcc	ccgtccgcac	ccccttgggc	cagaggatcc	gccgggcctt	cgtggccgag	1740
gcgggttggg	cgttggtggc	cctggactat	agccagatag	agctccgcgt	cctcgcccac	1800
ctctccgggg	acgaaaacct	gatcagggtc	ttccaggagg	ggaaggacat	ccacaccag	1860
accgcaagct	ggatgttcgg	cgtccccccg	gaggccgtgg	acccccctgat	gcgccggggc	1920
gccaagacgg	tgaacttcgg	cgtcctctac	ggcatgtccg	cccataggct	ctcccaggag	1980
cttgccatcc	cctacgagga	ggcgggtggc	tttatagagc	gctacttcca	aagcttcccc	2040
aaggtgcggg	cctggataga	aaagaccctg	gaggagggga	ggaagcgggg	ctacgtggaa	2100
accctcttcg	gaagaaggcg	ctacgtgccc	gacctcaacg	cccgggtgaa	gagcgtcagg	2160
gaggccgcgg	agcgcacggc	cttcaacatg	cccgtccagg	gcaccgccgc	cgacctcatg	2220
aagctcgcca	tggatgaagct	cttccccccg	ctccgggaga	tggggggccc	catgctcctc	2280
caggtcgcca	acgagctcct	cctggaggcc	ccccaaagcg	gggccgagga	ggtggcggct	2340

ttggccaagg aggccatgga gaaggcctat ccctcgccg tgccctgga ggtggaggtg 2400
 gggatggggg aggactggct ttccgccaag ggt 2433

<210> 588

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
 1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu
 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
 130 135 140

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
 145 150 155 160

Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
 420 425 430

Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 435 440 445

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 450 455 460

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510

Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525

Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575

Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605

Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620

Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640

Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
675 680 685

Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
690 695 700

Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
705 710 715 720

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
725 730 735

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
740 745 750

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
755 760 765

Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
770 775 780

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
785 790 795 800

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
805 810

<210> 589

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 589

atgaattccc tgccccctctt tgagcccaag ggccgggtcc tcctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca cctcccgggg ggagccggtg	120
cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcc accagacctc cgaggcctac	240
aaggcgggga gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300

ctggtggacc	tcttgggggt	tacccgcctc	gaggtccccg	gctacgaggc	ggacgacgtt	360
ctcgccaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtgcgcat	cctcaccgcg	420
gaccgggacc	tttaccagct	tctttccgac	cgcattcacg	tccttcaccc	cgaggggtac	480
ctcatcaccc	cggcctggct	ttgggaaaag	tacggcttga	ggcccgaacca	gtggggccgac	540
taccggggccc	tgaccgggga	cgaatccgac	aacctttccg	gggtcaaggg	catcggggag	600
aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
gaccggctga	agcccgccat	ccgggagaag	atcctggccc	acatggacga	tctgaagctc	720
tccttggagc	tctcccggtt	gcgcaccgac	ctccccctgg	aggtggactt	cgccaaaagg	780
cgggagcccc	accgggagag	gcttagggcc	tttctggaga	ggcttgagtt	tggcagcctc	840
ctccacgagt	tcgccccctt	ggaaagcccc	agggccgcgg	aggaagctcc	ctggccgccc	900
cccgagggag	ccttcgtggg	gtacgttctt	tcccgccccg	agcccatgtg	ggcggagctt	960
aacgccttgg	ccgccgccag	gggcggccgc	gtgcaccggg	cagcagaccc	cttggcgggg	1020
ctaaaggacc	tcaaggaggt	ccggggcctc	ctcgccaagg	acctcgccgt	cttggcctcg	1080
agggaggggc	tagacctcgt	gcccggggac	gaccccatgc	tcctcgcta	cctcctggac	1140
ccttcgaaca	ccacccccga	gggggtggcg	cggcgctacg	ggggggagtg	gacggaggac	1200
gccgcccacc	gggccctcct	ctcgagagag	ctccatcgga	acctccttaa	gcgcctcgag	1260
ggggaggaga	agctcctttg	gctctaccac	gaggtggaaa	agccctctc	ccgggtcctg	1320
gccccatatg	aggccaccgg	ggtacggcgg	gacgtggcct	accttcaggc	cctttccctg	1380
gagcttgccg	aggagatccg	ccgcctcgag	gaggaggtct	tccgcttggc	gggccacccc	1440
ttcaacctca	actcccggga	ccagctggaa	agggtgctct	ttgacgagct	taggttccc	1500
gccttgaaga	agacgaagaa	gacaggcaag	cgctccacca	gcgccgcggt	gctggaggcc	1560
ctacgggagg	cccaccccat	cgtggagaag	atcctccagc	accgggagct	caccaagctc	1620
aagaacacct	acgtggaccc	cctcccaagc	ctcgtccacc	cgaggacggg	ccgcctccac	1680
acccgcttca	accagacggc	cacggccacg	gggaggctta	gtagctccga	ccccaacctg	1740
cagaacatcc	ccgtccgcac	ccccttgggc	cagaggatcc	gccgggcctt	cgtggccgag	1800
gcgggttggg	cgttgggtgg	cctggactat	agccagatag	agctccgcgt	cctcgcccac	1860
ctctccgggg	acgaaaacct	gatcagggtc	ttccaggagg	ggaaggacat	ccacacccag	1920
accgcaagct	ggatgttcgg	cgtccccccg	gaggccgtgg	acccctgat	gcgccgggcg	1980
gccaagacgg	tgaacttcgg	cgtcctctac	ggcatgtccg	cccataggct	ctcccaggag	2040
cttgccatcc	cctacgagga	ggcgggtggc	tttatagagc	gctacttcca	aagcttcccc	2100
aaggtgcggg	cctggataga	aaagaccctg	gaggagggga	ggaagcgggg	ctacgtggaa	2160

accctcttcg gaagaaggcg ctacgtgccc gacctcaacg cccgggtgaa gagcgtcagg 2220
gaggccgcgg agcgcatggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg 2280
aagctcgcca tggatgaagct cttccccgcg ctccgggaga tgggggcccg catgctcctc 2340
caggtcgcca acgagctcct cctggaggcc ccccaagcgc gggccgagga ggtggcggt 2400
ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggagggtg 2460
gggatggggg aggactggct ttccgccaag ggt 2493

<210> 590

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 590

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe Ala Arg
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110

Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu

130		135		140
Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr				
145		150		155
				160
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp				
	165		170	175
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu				
	180		185	190
Ser Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu				
	195		200	205
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys				
	210		215	220
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu				
	225		230	235
Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp				
	245		250	255
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu				
	260		265	270
Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Pro Leu Glu				
	275		280	285
Ser Pro Arg Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala				
	290		295	300
Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu				
	305		310	315
Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp				
	325		330	335
Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala				
	340		345	350
Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro				
	355		360	365
Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr				
	370		375	380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400

Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
 405 410 415

Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
 420 425 430

Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
 435 440 445

Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
 450 455 460

Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495

Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
 500 505 510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525

Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540

Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His
 545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590

Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu
 595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620

Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln
 625 630 635 640

Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
660 665 670

Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
675 680 685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
690 695 700

Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu
705 710 715 720

Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
725 730 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
740 745 750

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
755 760 765

Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn
770 775 780

Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala
785 790 795 800

Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu
805 810 815

Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
820 825 830

<210> 591

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 591
agaaaggaag ggaagaaagc gaa 23

<210> 592

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 592
tggaggtcaa aacatcgata agtcgaagaa aggaagggaa gaaat 45

<210> 593

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 593
tgttttgacc tcca 14

<210> 594

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 594
ggcgaccaca cccgtcctgt 20

<210> 595

<211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 595
 ccacgatgcg tccggcgtag 20

 <210> 596
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 596
 acgggtcaat gtccatgccc caaaga 26

 <210> 597
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(23)
 <223> /note= "The residue at this position indicates 2' o-methyl sugar"

 <400> 597
 gtctgagatg aaagtgctcc cgcacccacc caaggcacag c 41

 <210> 598

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 598

tcttcgcaca tttcatctca gacgga

26

<210> 599

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(17)

<223> /note= "The residues at these positions are 2' o-methyl sugars"

<400> 599

gctgtgcctt ggggtggg

17

<210> 600

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (1)..(21)

<223> /note= "The residues at these positions are 2' o-methyls"

<400> 600

gctgtgcctt gggtaggtgc g

21

<210> 601

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 601

aacgaggcgc acccaccctaa ggcacagc

28

<210> 602

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (23)..(27)

<223> /note= "The residues at these positions are 2' o-methyls"

<400> 602

gtctgagatg aaagtgcgcc tcgttaa

27

<210> 603

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 603
aacgaggcgc acccacccaa ggcacagc

28

<210> 604

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 604
tcttcgcaca tttcatctca gac

23

<210> 605

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 605
gctgtgcctt gggtgggtgc g

21

<210> 606

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 606
tcttcgcaca tttcatctca gacgga 26

<210> 607

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 607
gctgtgcctt gggtgggtgc 20

<210> 608

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (15)..(20)

<223> /note= "The residues at these positions are 2' o-methyl sugars"

<400> 608
gctgtgcctt gggtgggtgc 20

<210> 609

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic
<220>
<221> modified_base
<222> (1)..(20)
<223> /note= "The residues at these positions are 2' o-methyl sugars"

<400> 609
gctgtgcctt gggtaggtgc 20

<210> 610
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 610
acgggtcaat gtccatgccc caaaga 26

<210> 611
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 611
aacgaggcgc acccacccaa ggcacagc 28

<210> 612
<211> 27
<212> DNA
<213> Artificial Sequence

```

<220>
<223> Synthetic
<220>
<221> modified_base
<222> (23)..(27)
<223> /note= "The residues at these positions are 2' o-methyls"

<400> 612
gtctgagatg aaagtgcgcc tcgttaa
27

<210> 613
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<220>
<221> modified_base
<222> (1)..(17)
<223> /note= "The residues at these positions are 2' o-methyls"

<400> 613
gctgtgcctt ggggtggg
17

<210> 614
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<220>

```


<221> modified_base
 <222> (1)..(19)
 <223> /note= "The residues at these positions are 2' o-methyls"

<400> 614
 gctgtgcctt ggggtgggtg 19

<210> 615
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> /note= "The residues at these positions are 2' o-methyls"

<400> 615
 gctgtgcctt ggggtgggtgc g 21

<210> 616
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(22)
 <223> /note= "The residues at these positions are 2' o-methyls"

<400> 616
gctgtgcctt ggggtgggtgc gc 22

<210> 617

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 617
ccgtcaacat ttaccatggg tgcgga 26

<210> 618

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 618
ccgccacctc gtagtcgaca tccttttcgt g 31

<210> 619

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 619
ttgataaatt tgggggtggaa aggtttgga 29

<210> 620

<211> 17

<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 620
agaactgaga ggaggcg

17

<210> 621

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 621
aacgaggcgc accaaactca ctcac

25

<210> 622

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 622
gtcatgtagg cttctatgta gttgatgaag atgta

35

<210> 623

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic	
<400> 623	
ggctttgtag atgcctttct cttgga	26
<210> 624	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 624	
atgagtgagt ttggtgcg	18
<210> 625	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 625	
ccaggaagca agtggtgcgc ctcgttt	27
<210> 626	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 626	
aacgaggcgc accttgagg ca	22
<210> 627	

<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 627
aaggtttcct tctcagttgt gtta

24

<210> 628
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 628
gcaaagatgt ctgttacggt caactc

26

<210> 629
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 629
tgcctccaag gtgcgc

16

<210> 630
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 630
 aacgaggcgc accttcaaaa tgcctaa 27

 <210> 631
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 631
 tgtcactctc ctctttccaa tta 23

 <210> 632
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 632
 gaaaagagtt ccattatccg ctacatctg 29

 <210> 633
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 633
 ttaggcattt tgaagggtgcg c 21

<210> 634
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 634
aacgaggcgc accgttgtgt ccc

23

<210> 635
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 635
gggatgtaga agccattcag a

21

<210> 636
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 636
ttgttgtgct gtgggggatg

20

<210> 637
<211> 17
<212> DNA
<213> Artificial Sequence

<220>		
<223>	Synthetic	
<400>	637	
	gggacacaac ggtgcgc	17
<210>	638	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	638	
	ccgtcacgcc tccaccatat ccc	23
<210>	639	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	639	
	ccagcggttt ccattggcaa agatcaa	27
<210>	640	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	640	
	cggaagaatg ggtagccat g	21

<210> 641
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 641
gggatatggt ggaggcg

17

<210> 642
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 642
aacgaggcgc accgttccag gc

22

<210> 643
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 643
catatccatg cagcaccacc atga

24

<210> 644
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 644

caaaatacag agtgaacaca gggcc

25

<210> 645

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 645

gcctggaacg gtgcgc

16

<210> 646

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 646

ccgtcacgcc tcatggataa tgccc

25

<210> 647

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 647

caggtgagaa aaggcattac agatagtgaa agc

33

<210>	648	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	648	
	cagaggaaag agagctgcag gg	22
<210>	649	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	649	
	gggcattatc catgaggcg	19
<210>	650	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	650	
	ccgtcacgcc tccctgctga gaaa	24
<210>	651	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	

<220>		
<223>	Synthetic	
<400>	651	
	cccgaggcat gcacggcgga	20
<210>	652	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	652	
	ggcaggaagg cctcc	15
<210>	653	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	653	
	tttctcagca gggaggcg	18
<210>	654	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	654	
	ccgtcacgcc tcgccccaca	20

<210>	655	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	655	
	cagcacaggc tggtgaccat cataaaac	28
<210>	656	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	656	
	ctttccata ctttttatga cattc	25
<210>	657	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	657	
	tgtggggcga ggcg	14
<210>	658	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	

<220>	
<223>	Synthetic
<400>	658
aacgaggcgc	acagttgacc ttc
	23
<210>	659
<211>	19
<212>	DNA
<213>	Artificial Sequence
<220>	
<223>	Synthetic
<400>	659
gtgatggcca	gcacagggc
	19
<210>	660
<211>	20
<212>	DNA
<213>	Artificial Sequence
<220>	
<223>	Synthetic
<400>	660
atacgttccc	cacatttttc
	20
<210>	661
<211>	18
<212>	DNA
<213>	Artificial Sequence
<220>	
<223>	Synthetic
<400>	661
tgaaggtcaa	ctgtgcgc
	18

<210> 662
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 662
 aacgaggcgc acgtcataaa tacccc

26

<210> 663
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 663
 gccagcatag gctgttgaca c

21

<210> 664
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 664
 agacttttct atacttttta taacattc

28

<210> 665
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic
<400> 665
gggggtattta tgacgtgcgc 20

<210> 666
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 666
ccgtcacgcc tcctgtctgt gat 23

<210> 667
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 667
tcctgacagt gctcaatcag ga 22

<210> 668
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 668
tcctgacaat gctcaatgag ga 22

<210> 669
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 669
gtcccggatg tggccc

16

<210> 670
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 670
atcacagaca ggaggcg

17

<210> 671
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 671
aacgaggcgc acggactgtt ttctgc

26

<210> 672
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 672
 cttgtcaaag tcctgatagt gtcctc 27

 <210> 673
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 673
 cttgttgaag tcctgatagt gtcctc 27

 <210> 674
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 674
 gcagaaaaca gtccgtgcgc 20

 <210> 675
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 675
 ccgtcacgcc tcaactgcgt cat 23

<210>	676	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	676	
	gtggataact gcatcagtgt atggcatttt c	31
<210>	677	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	677	
	caaggggttg tagcctgtgt gagcc	25
<210>	678	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	678	
	atgaccgcag tgaggcg	17
<210>	679	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	

<220>
 <223> Synthetic
 <400> 679
 ccgtcacgcc tcagagccaa tcac 24

 <210> 680
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 680
 cgatcatcaa gggatggtgg cctgtgc 27

 <210> 681
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 681
 ctgatcaatc tccttttgga ctttctctgc g 31

 <210> 682
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 682
 gtgattggct ctgaggcg 18

<210> 683
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 683
ccgtcacgcc tcctcttcaa tttctg

26

<210> 684
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 684
ccctgtcaat ttcttcatga agttta

26

<210> 685
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 685
ggtatttcat gaggatcagg agc

23

<210> 686
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 686
 cagaaattga agaggaggcg 20

 <210> 687
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 687
 aacgaggcgc accgggtccc a 21

 <210> 688
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 688
 tcccctgttt cttgaaaagt ccatgtgtga 30

 <210> 689
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 689
 aatccgtaga ggagcaccag g 21

<210> 690
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 690
tgggacccgg tgcgc

15

<210> 691
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 691
ccgtcacgcc tcctcggcag g

21

<210> 692
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 692
cacaatatcg taggtaggag gtgccttaa

29

<210> 693
<211> 18
<212> DNA
<213> Artificial Sequence

<220>		
<223>	Synthetic	
<400>	693	
	gccccatcga tctcctcc	18
<210>	694	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	694	
	cctgccgagg aggcg	15
<210>	695	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	695	
	aacgaggcgc actaggcttt gct	23
<210>	696	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	696	
	ttcatgtagt cagggtcata gacaattaag a	31

<210> 697
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 697
tccccagaac catcgaggaa agg

23

<210> 698
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 698
agcaaagcct agtgcgc

17

<210> 699
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 699
aacgaggcgc acagaaggcc cctt

24

<210> 700
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 700
 ccttgaacag caccagaaat agactgagca c 31

<210> 701
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 701
 ggaagaaccc agagacacca tcc 23

<210> 702
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 702
 aaggggcctt ctgtgcgc 18

<210> 703
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 703
 aacgaggcgc acgttgtgat acctt 25

<210>	704	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	704	
	gatgaaggcc ataaattaaa attgtgc	27
<210>	705	
<211>	16	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	705	
	tgggtatgga acgtcc	16
<210>	706	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	706	
	aaggtatcac aacgtgcgc	19
<210>	707	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	

<220>		
<223>	Synthetic	
<400>	707	
	cccccttttg gggg	14
<210>	708	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	708	
	ccctatcttt aaagttttta aaaagtttga	30
<210>	709	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	709	
	ccgccgagat cactctgact gcct	24
<210>	710	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	710	
	ttgtcactcg gggttcgaga agatgaa	27

<210>	711	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	711	
	gggccagagg gctgattag	19
<210>	712	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	712	
	gggccagagg gctgatta	18
<210>	713	
<211>	16	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	713	
	gggccagagg gctgat	16
<210>	714	
<211>	13	
<212>	DNA	
<213>	Artificial Sequence	

<220>		
<223>	Synthetic	
<400>	714	
	gggccagagg gct	13
<210>	715	
<211>	11	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	715	
	gggccagagg g	11
<210>	716	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	716	
	aggcagtcag agtgatc	17
<210>	717	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	717	
	aggcagtcag agtgatctc	19

<210> 718
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 718
cggaagaagc agttggtgat ctcggcgg

28

<210> 719
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 719
caacgcttcc tccg

14

<210> 720
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 720

ccgtcacgcc tctctgactg cct 23

<210> 721

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 721

ttgtcactcg gggttcgaga agatgaa 27

<210> 722

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 722

gggccagagg gctgattag 19

<210> 723

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 723

aggcagtcag agaggcg 17

<210> 724

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 724

cggaagaagc agttggaggc gtgacggt

28

<210> 725

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 725

caacgcttcc tccg

14

<210> 726

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 726

ccgtcaagcc tctctgactg cctgg

25

<210> 727

<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 727
ttgtcactcg gggttcgaga agatgaa

27

<210> 728
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 728
ccaggcagtc agagaggcg

19

<210> 729
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 729
cggaagaagc agttggaggc gtgacggt

28

<210> 730
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic
<220>
<221> misc_feature
<222> (4)..(4)
<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 730
caacgcttcc tccg 14

<210> 731
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 731
ccgccgagat cactctgact gcc 23

<210> 732
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 732
ttgtcactcg gggttcgaga agatgaa 27

<210> 733
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 733
 tgggccagag ggctgatta 19

 <210> 734
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 734
 aggcagtcag agtgatc 17

 <210> 735
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 735
 cggaagaagc agttggtgat ctcggcgg 28

 <210> 736
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 736

caacgcttcc tccg

14

<210> 737

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 737

ccgccgagat cactgatctg actg

24

<210> 738

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 738

cttgctcactc ggggttcgag aagac

25

<210> 739

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 739

cctgggccag agggctgatt 20

<210> 740

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 740

cagtcagatc agtgatc

17

<210> 741

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 741

cggaagaagc agttggtgat ctcggcgg

28

<210> 742

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 742	
caacgcttcc tccg	14
<210> 743	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 743	
ccgtcacgcc tctctgactg cca	23
<210> 744	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 744	
ccgtcacgcc tctctgactg ccg	23
<210> 745	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 745	
ccgtcacgcc tctctgacgg cct	23
<210> 746	
<211> 23	

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 746
 ccgtcacgcc tctctgacag cct 23

 <210> 747
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 747
 ttgtcactcg gggttcgaga agatgaa 27

 <210> 748
 <211> 11
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 748
 gggccagagg g 11

 <210> 749
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic	
<400> 749	
aggcagtcag agaggcg	17
<210> 750	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 750	
aggccgtcag agaggcg	17
<210> 751	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 751	
aggctgtcag agaggcg	17
<210> 752	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 752	
ccaggaagca agtggaggcg tgacggu	27
<210> 753	

<211> 13
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.

 <400> 753
 cactgcttcg tgg 13

 <210> 754
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 754
 ccgccgagat cactctgatg cctggg 26

 <210> 755
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 755
 cttgtcactc ggggttcgag aagatgaa 28

<210> 756
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 756
 cccaggcagt cagagtgatc 20

 <210> 757
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 757
 cggaggaagc agttggtgat ctcggcgg 28

 <210> 758
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye.

 <400> 758

caacgcttcc tccg 14

<210> 759

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 759

ccgtcacgcc tccatctggt taggg 25

<210> 760

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 760

caggtcctgg aaggagcact ta 22

<210> 761

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 761

ccatcagctt ctttgttctt gtcac 26

<210> 762

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 762

gccctaaca gatggaggcg

20

<210> 763

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 763

cgaagaagc agtggaggc gtgacggt

28

<210> 764

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 764

caacgcttcc tccg

14

<210> 765

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 765

ccgtcacgcc tccatctggt tagggc

26

<210> 766

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 766

caggtcctgg aaggagcact ta

22

<210> 767

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 767

catcagcttc tttgttcttg tcatcc

26

<210> 768

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic	
<400> 768	
gccctaaaca gatggaggcg	20
<210> 769	
<211> 28	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 769	
cggagaagc agttggaggc gtgacggt	28
<210> 770	
<211> 14	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 770	
caacgcttcc tccg	14
<210> 771	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 771	
ccgtcacgcc tccatctggt tagg	24
<210> 772	

<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 772
caggctcctgg aaggagcact ta

22

<210> 773

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 773
gccatcagct tctttgttct tgtcatc

27

<210> 774

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 774
cggaagaagc agttggaggc gtgacggc

28

<210> 775

<211> 14

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic
<220>
<221> misc_feature
<222> (4)..(4)
<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 775
caacgcttcc tccg 14

<210> 776
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 776
ccgtcacgcc tcccatcagc ttc 23

<210> 777
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 777
gagcacttca tctgttttagg ga 22

<210> 778
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 778

tttgttcttg tcatcctcat tgccac

26

<210> 779

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 779

gaagctgatg ggaggcg

17

<210> 780

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 780

cggaagaagc agttggaggc gtagcggc

28

<210> 781

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature
<222> (4)..(4)
<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 781
caacgcttcc tccg 14

<210> 782
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 782
ccgccgagat cactcatctg tttagggcc 29

<210> 783
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
<400> 783
ccgccgagat cactcatctg tttagggc 28

<210> 784
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 784
caggtcctgg aaggagcact a 21

<210> 785

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 785
ggccctaaac agatgagtga tc 22

<210> 786

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 786
cggaggaagc agttggtgat ctcggcgg 28

<210> 787

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)...(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 787
caacgcttcc tccg 14

<210> 788

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 788
ccgtcacgcc tccagcaggt tggc 24

<210> 789

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 789
gcttgaccca gggaggg 17

<210> 790

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 790
gccaaggtgc tggaggcg 18

<210> 791

<211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 791
 cggaagaagc agttggaggc gtgacggt 28

 <210> 792
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye.

 <400> 792
 caacgcttcc tccg 14

 <210> 793
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 793
 ccgtcacgcc tccagcaggt tgg 23

<210> 794
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 794
gcttgaccca gggaggg

17

<210> 795
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 795
caatctcggg ctgcaaagca gac

23

<210> 796
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 796
gccaaggtgc tggaggcg

18

<210> 797
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 797
 cggaagaagc agttggaggc gtgacggt 28

 <210> 798
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye.

 <400> 798
 caacgcttcc tccg 14

 <210> 799
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 799
 ccgtcacgcc tctcagcagg ttgg 24

 <210> 800
 <211> 22
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 800

actctagttt ttccttctcc ta

22

<210> 801

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 801

caatctcggt ctgcaaagca gac

23

<210> 802

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 802

ccaacctgct gagaggcg

18

<210> 803

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 803
cggaagaagc agttggaggc gtgacggt

28

<210> 804

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 804
caacgcttcc tccg

14

<210> 805

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 805
ccgccgagat cactctcctc attgaatcct

30

<210> 806

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic
 <400> 806
 ccgccgagat cactctcctc attgaatcc 29
 <210> 807
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 807
 ccaaaagtcc agtgatgatt ttcaccaggc aaga 34
 <210> 808
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 808
 aggattcaat gaggaagagt gatct 25
 <210> 809
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 809
 cggaggaagc agttggtgat ctcggcgg 28
 <210> 810

<211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 810
 caacgcttcc tccg 14

<210> 811
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 811
 ccgtcacgcc tcctcctcat tgaa 24

<210> 812
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 812
 ccagtgatga ttttcaccag gcaagta 27

<210> 813
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 813
tccagattgg aagcatccat ct

22

<210> 814
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 814
ttcaatgagg aggaggc

17

<210> 815
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 815
cggaagaagc agttggaggc gtgacggt

28

<210> 816
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 816
 caacgcttcc tccg 14

<210> 817
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 817
 ccgtcacgcc tcctcctcat tga 23

<210> 818
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 818
 ccagtgatga ttttcaccag gcaagta 27

<210> 819
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 819

atccagattg gaagcatcca tct

23

<210> 820

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 820

ttcaatgagg aggaggc

17

<210> 821

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 821

cggaagaagc agttggaggc gtagcgg

28

<210> 822

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 822

caacgcttcc tccg

14

<210> 823

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 823

ccgtcacgcc tcctcctcat tgaatg

26

<210> 824

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 824

ccgtcacgcc tcctcctcat tgaata

26

<210> 825

<211> 26

<212> DNA

<213> Artificial Sequence

<220>